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(54) Title: METHODS FOR IDENTIFYING MARKER GENES FOR CANCER

(57) Abstract: The invention describes a method of identifying tissue-specific tumor markers and diagnostic and therapeutic methods and compositions of using the same. More specifically, the invention presents a method for a rational search of diagnostic and prognostic cancer markers and therapeutic targets among the genes negatively regulated by tumor suppressor genes.

## METHODS FOR IDENTIFYING MARKER GENES FOR CANCER

### Field of the Invention

5           The invention relates generally to the field of cancer. More specifically, the invention details methods for the identification of markers specific for one or several types of cancer, depending on tissue origin. Such markers are useful in numerous diagnostic and prognostic applications as well as cancer type-specific targets for therapeutic intervention.

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### Background of the Invention

          An effective cure of any given cancer will greatly depend on the development of new diagnostic assays based on identification of reliable serological and histological markers and on designing new therapeutic strategies and  
15       pharmaceuticals for effective elimination of cancer cells in the diseased individual. Tumor suppressor genes normally function to inhibit division or survival of genetically damaged cells and thus function to prevent the development of tumors. Mutations in tumor suppressor genes cause the cell to ignore one or more of the components of a network of inhibitory signals, removing the inhibitory mechanisms  
20       from the cell cycle, and resulting in a higher rate of uncontrolled growth, *i.e.*, cancer. Tumor suppressor genes are defined by the impact of their absence and thus tend to be recessive. Thus, neoplasia is the result of the loss of function of these genes. The loss or inactivation of a normal tumor suppressor gene may be acquired somatically in a single clone of cells or be constitutionally present throughout the body, including the  
25       germ line.

          There are numerous tumor suppressors known to those of skill in the art, including, for example, p53; the retinoblastoma gene, commonly referred to as Rb1; the adenomatous polyposis of the colon gene (APC); familial breast/ovarian cancer gene 1 (BRCA1); familial breast/ovarian cancer gene 2 (BRCA2); CDH1  
30       cadherin 1 (epithelial cadherin or E-cadherin) gene; cyclin-dependent kinase inhibitor 1C gene (CDKN1C, also known as p57, KIP2 or BWS); cyclin-dependent kinase inhibitor 2A gene (CDKN2A also known as p16 MTS1 (multiple tumor suppressor 1), TP16 or INK4); familial cylindromatosis gene (CYLD; formerly known as EAC

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(epithelioma adenoides cysticum)); E1A-binding protein gene (p300); multiple exostosis type 1 gene (EXT1); multiple exostosis type 2 gene (EXT2); homolog of *Drosophila* mothers against decapentaplegic 4 gene (MADH4; formerly referred to as DPC4 (deleted in pancreatic carcinoma 4) or SMAD4 (SMA- and MAD-related protein 4)); mitogen-activated protein kinase kinase 4 (MAP2K4; also referred to as JNKK1, MEK4, MKK4, or PRKMK4; formerly known as SEK1 or SERK1); multiple endocrine neoplasia type 1 gene (MEN1); homolog of *E. coli* MutL gene (MLH1 also known as HNPCC (hereditary non-polyposis colorectal cancer) or HNPCC2; formerly referred to as COCA2 (colorectal cancer 2) and FCC2); homolog of *E. coli* MutS 2 gene (MSH2 also called HNPCC (hereditary non-polyposis colorectal cancer) or HNPCC1 and formerly known as COCA1 (colorectal cancer 1) and FCC1); neurofibromatosis type 1 gene (NF1); neurofibromatosis type 2 gene (NF2); protein kinase A type 1, alpha, regulatory subunit gene (PRKAR1A, formerly known as PRKAR1 or TSE1 (tissue-specific extinguisher 1)); homolog of *Drosophila* patched gene (PTCH; also called BCNS); phosphatase and tensin homolog gene (PTEN, also called MMAC1 (mutated in multiple advanced cancers 1), formerly known as BZS (Bannayan-Zonana syndrome) and MHAM1 (multiple hamartoma 1)); succinate dehydrogenase cytochrome B small subunit gene (SDHD; also called SDH4); Swi/Snf5 matrix-associated actin-dependent regulator of chromatin gene (SMARCB1, also referred to as BAF47, HSNFS, SNF5/INI1, SNF5L1, STH1P, and SNR1); serine/threonine kinase 11 gene (STK11 also known as LKB1 and PJS); tuberous sclerosis type 1 gene (TSC1 also known as KIAA023); tuberous sclerosis type 2 gene (TSC2, previously referred to as TSC4); von Hippel-Lindau syndrome gene (VHL); and Wilms tumor 1 gene (WT1, formerly referred to as GUD (genitourinary dysplasia), WAGR (Wilms tumor, aniridia, genitourinary abnormalities, and mental retardation), or WIT-2), DAP-kinase, FHIT, Werner syndrome gene, and Bloom syndrome gene.

The p53 tumor suppressor gene is an exemplary tumor suppressor in its mode of action. It encodes a nuclear transcription factor that accumulates in cells in response to a variety of stresses, thereby inducing growth arrest or apoptosis (Gottlieb and Oren, *Biochim Biophys Acta.*, 1287(2-3):77-102 (1996). p53 or the pathway mediated by p53 are inactivated in the majority of human tumors, including advanced prostate cancer (Steele *et al.*, *Br J Surg.*, 85(11):1460-1467 (1998); Ozen and Pathak, *Anticancer Res.*, 20(3B):1905-1912 (2000).

One of the functions of the p53 protein in the cell is that it binds DNA stimulating the expression of p21-waf1 that interacts with a cell division-stimulating protein (cdk2). When p21 is complexed with cdk2, the cell cannot pass to the S stage of cell division (G1 check point). Mutant p53 can no longer bind DNA in an effective way, and as a consequence the p21-waf1 protein is not made available to act as the 'stop signal' for cell division. Thus, cells divide uncontrollably and form tumors. Thus, inactivation of p53 is associated with the loss of this cell cycle checkpoint control and with the consequent resistance to anti-cancer treatment, genomic instability, and enhanced angiogenesis, leading to rapid tumor progression (Gottlieb and Oren, *Biochim Biophys Acta.*, 1287(2-3):77-102 (1996); Cordon-Cardo *et al.*, *Semin. Surg. Oncol.*, 13:319-327 (1997).

Many p53-mediated effects are achieved through the activity of p53-responsive genes that are either up- or down-regulated by p53. In fact, the activity of p53-responsive genes account, in part, for p53-mediated checkpoint control [upregulation of p21-waf1, 14-3-3  $\square$  (G2 checkpoint)], apoptosis (upregulation of bax, PUMA, and genes determining enhanced reactive oxygen species metabolism), suppression of angiogenesis (upregulation of thrombospondins 1 and 2, and downregulation of VEGF) and p53 feedback regulation (upregulation of mdm2) (see Gottlieb and Oren, *Biochim Biophys Acta.*, 1287(2-3):77-102 (1996) for references). Much like p53, the other tumor suppressors listed above also mediate their effects through the activity of responsive genes that are either up- or down-regulated by the tumor suppressor, directly or indirectly. Genes that have altered expression in tumors may serve as targets for development of anti-cancer drugs, or cancer markers or both. However, the relationship between changes in gene expression, resulting from tumor suppressor deficiency, and tumor progression is not sufficiently understood. It also remains unclear why the germline loss of tumor suppressor gene function leads to development of certain specific types of cancer and not others. This implies that in each specific tissue the changes in gene expression imposed by the loss of tumor suppressor gene are unique. Taking into account a need for tissue-specific markers of cancer, the inventors have devised a method for the identification of such tissue-specific markers by exploiting the tumor suppressor regulation of genes in cancer cells.



### Summary of the Invention

The invention relates to methods for diagnosing and prognosing cancer by utilizing general as well as tissue-specific genetic markers, methods for identifying these markers, and the markers identified by such methods.

5 The invention provides a method of identifying tissue-specific and general tumor markers and diagnostic and therapeutic methods and compositions of using the same. Diagnostic markers may be screening markers (secreted polypeptides), histological markers (using which it is possible to distinguish tumor tissue from benign tissue within histological samples) or staging markers  
10 (determining the stage of a cancer by detection of the presence of specific cancer cells in blood (micrometastases) by RT-PCR on identified cancer-type-specific markers on the whole blood RNA).

The invention provides a method of identifying a diagnostic marker for a cancer comprising: a) obtaining a first cell from a first cell type of the cancer, the  
15 cell comprising a defective tumor suppressor expression; b) obtaining a second cell of the first cell type, wherein the second cell comprises a wild-type tumor suppressor expression; c) identifying genes having an increased level of expression in the first cell as compared to the second cell; and d) selecting at least one gene of step c) as a diagnostic marker for the cancer.

20 In the diagnostic and therapeutic methods for using such a marker(s), the invention provides a method of diagnosing a cancer in a subject comprising determining, in a sample from the subject, the level of at least one polypeptide, wherein a higher level of the polypeptide compared to the level of the polypeptide in a subject free of cancer is indicative of cancer, and wherein the polypeptide is selected  
25 from the group consisting of a) polypeptides encoded by the polynucleotides listed in Table 5 or in Table 6; and b) polypeptides which are at least 70% homologous to the polypeptides of a) at the amino acid sequence level. In one embodiment of the diagnostic methods, the level of a polypeptide-encoding polynucleotide is determined, rather than the polypeptide itself. In such methods, the invention contemplates any of  
30 the polynucleotides in Table 6, polynucleotides having sequences that differ from the polynucleotides in a) without changing the polypeptide encoded thereby, and polynucleotides that are at least 70% homologous to the polynucleotides of a) at the nucleic acid sequence level.

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In the case of at least p53 and possibly other tumor suppressors, the invention further provides a method of determining the p53 status within the tumor (*i.e.*, whether the cancer cell is a p53<sup>-</sup> or a p53<sup>+</sup> tumor cell.), which is important for prognosis and treatment selection.

5           The invention also provides a method for monitoring the activity of p53 suppressive drugs, or drugs that suppress other tumor suppressors described herein, by measuring any of the markers identified herein the polypeptides of which are secreted, such as PSA or pancreatitis-associated protein. In this aspect, the invention provides a method of measuring the responsiveness of a subject to a cancer  
10 treatment comprising determining the level of at least one polypeptide in a sample taken from the subject before treatment, and comparing it with the level of the polypeptide in a sample taken from the subject after treatment, a decrease in the level indicating responsiveness of the subject to the cancer treatment, wherein the polypeptide is selected from the group consisting of a) polypeptides encoded by the  
15 polynucleotides listed in Table 5 and Table 6; and b) polypeptides which are at least 70% homologous to the polypeptides of a).

In a related aspect, the invention provides a method of measuring the responsiveness of a subject to a cancer treatment comprising determining the level of at least one polypeptide-encoding polynucleotide in a sample taken from the subject  
20 before treatment, and comparing it with the level of the polynucleotide in a sample taken from the subject after treatment, a decrease in the level indicating responsiveness of the subject to the cancer treatment, wherein the polynucleotide is selected from the group consisting of: a) the polynucleotides listed in Table 6; b) polynucleotides having sequences that differ from the polynucleotides in a), without  
25 changing the polypeptide encoded thereby; and c) polynucleotides which are at least 70% homologous to the polynucleotides of a).

According to another aspect of the invention, a method is provided of screening for drugs useful in the treatment of cancer. A cell which harbors a tumor suppressor mutation or defective expression is contacted with a test substance.  
30 Expression of a transcript or its translation product is monitored. The transcript is a tissue-specific tumor marker of the invention. A test substance is identified as a potential drug for treating cancer if it decreases expression of a marker identified as one that is up-regulated as a result of loss of tumor suppressor function. Alternatively,

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the test substance is identified as a potential drug if it increases the expression of a marker identified as one that is down regulated as a result of loss of tumor suppressor function.

For example, the invention provides a method for screening for  
5 compounds that modulate the activity of a tumor suppressor gene comprising a) obtaining a cell comprising a defective tumor suppressor expression; b) measuring the level of expression of a marker of Table 5 or 6 in the cell; c) contacting the cell with a test compound; and d) measuring the expression of the marker of step b) after the contacting step c), wherein a change in the level of expression after the contacting  
10 step as compared to the level of expression before the contacting step is indicative of the ability of the compound to modulate the activity of the tumor suppressor gene.

Another aspect of the invention concerns a method of determining p53 inactivation in prostate cells of an individual comprising determining the levels of serum PSA, wherein elevated serum PSA levels in said individual are indicative of  
15 p53 inactivation in said prostate cells.

Yet another aspect of the invention a method of monitoring the effect of a p53-based cancer therapy on a prostate cancer patient, the prostate cancer cells of said patient having a p53 loss of function mutation, said method comprising determining the levels of serum PSA of said patient before and after said therapy,  
20 wherein a decrease in the serum PSA levels after provision of said therapy is indicative of said therapy overcoming the deleterious effects of said p53 mutation.

In addition, the invention also contemplates a method of detection of p53 inactivation in other tissues. For example, from observations of pancreatitis associated protein, the inactivation of p53 in pancreatic carcinoma may be  
25 determined. Similar observations may be made about other preferred markers disclosed in this application.

Numerous other aspects and advantages of the invention will be apparent upon consideration of the following drawings and detailed description.

30

### Brief Description of the Drawings

The following drawings form part of the present specification and are included to further illustrate aspects of the invention. The invention may be better

understood by reference to the drawings in combination with the detailed description of the preferred embodiments presented herein.

Figure 1: Inactivation of p53 pathway in LNCaP cells by GSE56 correlates with increased secretion of PSA. Quantitation of PSA protein in culture medium conditioned by the indicated cells, performed by the Microparticle Enzyme Immunoassay method using IMx operation system (Abbott Diagnostics, Abbott Park, IL, USA) binding to DNA for repression (Kley *et al.*, *Nucleic Acids Res.*, 20:4083-4087 (1992); Sun *et al.*, *J. Biol. Chem.*, 274:11535-11540 (1999); Xu *et al.*, *Oncogene*, 19:5123-5133 (2000).

Figure 2: Opposite regulatory effect of p53 on PSA and p21 promoters. Chloramphenicol acetyltransferase (CAT)-reporter constructs were used to estimate p53 influence on PSA and p21 promoter elements. A panel of reporter constructs: pBasic-CAT (CAT gene under minimal thymidine kinase promoter), pWAF1-CAT (p53-binding site from p21/Waf1 gene upstream of the minimal thymidine kinase promoter); p407ECAT plasmid, containing 1.6 kb enhancer (-5322 to -3740) and 418 bp promoter (-407 to +11) elements from PSA gene followed by promoterless CAT (Zhang *et al.*, *Biochem. Biophys. Res. Comm.*, 231:784-788 (1997); Zhang *et al.*, *Nucleic Acids Res.*, 25:3143-3150 (1997) were transfected into LNCaP cells in combination with different amounts of pLp53SN, containing human wild type p53, pLGSE56SN expressing GSE56 or empty pLXSN vector using Lipofectamin Plus reagent (Gibco BRL). Bars reflect relative CAT activity in lysates of LNCaP cells transiently transfected with either PSA-CAT (upper panel) or p21-CAT (lower panel) constructs in combination with the indicated plasmids. Results are normalized according to transfection efficiency and CAT expression in control cells transfected with insert-free vector. wt, plasmid expressing wild type human p53 cDNA; GSE, plasmid. (1) and (2) indicate plasmid concentration in micrograms. The experiment was repeated three times and showed similar results with variations in relative CAT activity values less than 20 percent.

Figure 3: Trichostatin A (TSA) treatment eliminates the effect p53 has on PSA promoter activity. Bars show relative CAT activity in lysates of LNCaP cells transiently transfected with the indicated plasmid DNAs. TSA (100 nM) was added 5 h and CAT activity was measured 40 h post-transfection. Values reflect average of three independent experiments normalized according to transfection efficiency and CAT expression in control cells transfected with insert-free vector with no TSA.

156Pro mutants had no detectable effect on PSA. Thus, the dominant negative activity of tumor-derived p53 mutants is well correlated with the increased production of PSA by LNCaP cells, suggesting that similar events occur during tumor progression.

Figure 4: Effect of tumor-derived p53 mutants on the levels of p21 protein expression and on PSA secretion by LNCaP cells. LNCaP cells were transduced with insert-free retrovirus or retroviruses expressing indicated p53 mutants. A panel of constructs expressing p53 mutants (pPS-p53<sup>135val</sup>, pPS-p53<sup>141Ala</sup>, pPS-p53<sup>156Pro</sup>, pPS-p53<sup>175His</sup>) was prepared in Mo- MuLV-based retroviral vector pPS-Hygro, expressing the p53 cDNA under the control of LTR and the hygromycin resistance gene under the control of SV40 promoter (Ossovskaia *et al.*, *Proc. Natl. Acad. Sci. USA*, 93:10309-10314 (1996). Expression of p53 and p21 proteins was detected in the lysates of untreated LNCaP cell populations by Western immunoblotting with appropriate antibodies. Before loading, samples were normalized according to protein amounts confirmed by membrane staining and probing with anti-actin antibodies. 24-hour medium was collected from the same cell cultures and amounts of PSA protein were measured by Microparticle Enzyme Immunoassay, using IMx operation system (Abbott Diagnostics, Abbott Park, IL, USA).

Figure 5 contains the sequences of the genes listed in Tables 5 and 6, in order of the sequence ID number (SEQ ID NO). Note that the GenBank accession Number of the mouse EST printed on the chip is given in the tables; the name of the corresponding human consensus sequence [mRNA] (obtained by bioinformatic analysis) and the GenBank ID(s) of the sequence closest to the consensus sequence, where available, was added into Tables 5 and 6. Figure 5 contains the human consensus sequence of each gene, where available, or the mouse consensus sequence, if the human sequence was unavailable, or the mouse EST sequence, if neither human nor mouse consensus sequence was available. The sequence identifier (SEQ ID NO), and corresponding Genbank accession number, are denoted before each sequence.

This application contains six Excel tables (Table 1-6 discussed herein). These tables are attached to this application as printed tables and also on a diskette.

### Detailed Description of the Preferred Embodiments

The invention deals with methods of obtaining genetic markers for diagnosis and prognosis of cancer and methods for the use of these markers.

A preferred embodiment of the diagnostic aspect concerns a method of diagnosing a cancer in a subject comprising determining, in a sample from the subject, the level of at least one polypeptide, wherein a higher level of the polypeptide compared to the level of the polypeptide in a subject free of cancer is indicative of cancer, and wherein the polypeptide is selected from the group consisting of: polypeptides encoded by the human polynucleotides or the human orthologs of mouse polynucleotides listed in Table 5 or 6, and homologs of said polypeptides having at least 70% homology, preferably at least 80% homology, more preferably at least 90% homology.

The sample may be taken from a bodily fluid, such as blood, lymph fluid, ascites, serous fluid, pleural effusion, sputum, cerebrospinal fluid, lacrimal fluid, synovial fluid, saliva, stool, sperm and urine. The sample may also originate from a tissue, such as brain, lung, liver, spleen, kidney, pancreas, intestine, colon, mammary gland or breast, stomach, prostate, bladder, placenta, uterus, ovary, endometrium, testicle, lymph node, skin, head or neck, esophagus, bone marrow, and blood or blood cells.

General protocols for the detection of cancer markers can be found in "Tumor Marker Protocols", Hanausek & Walaszek (Eds.), Humana Press, 1998. Methods of determining the level of a polypeptide in a sample are well known in the art (see, for example: Coligan et al, Unit 9, Current Protocols in Immunology, Wiley Interscience, 1994) and include, *inter alia*: immunohistochemistry (Microscopy, Immunohistochemistry and Antigen Retrieval Methods: For Light and Electron Microscopy, M.A. Hayat (Author), Kluwer Academic Publishers, 2002; Brown C.: "Antigen retrieval methods for immunohistochemistry", *Toxicol Pathol* 1998; 26(6): 830-1; ELISA (Onorato et al., "Immunohistochemical and ELISA assays for biomarkers of oxidative stress in aging and disease", *Ann NY Acad Sci* 1998 20; 854: 277-90), western blotting (Laemmli UK: "Cleavage of structural proteins during the assembly of the head of a bacteriophage T4", *Nature* 1970;227: 680-685; Egger & Bienz, "Protein (western) blotting", *Mol Biotechnol* 1994; 1(3): 289-305), antibody microarray hybridization (Huang, "detection of multiple proteins in an antibody-based protein microarray system, *Immunol Methods* 2001 1; 255 (1-2): 1-13) and Targeted molecular imaging, which can be carried out on the whole body with imaging agents such as antibodies against the marker polypeptides (which may be membrane-bound proteins), the marker polypeptides themselves, receptors and contrast agents. The

visualizations techniques include single photon and positron emission tomography, magnetic resonance imaging (MRI), computed tomography or ultrasonography (Thomas, Targeted Molecular Imaging in Oncology, Kim et al (Eds), Springer Verlag, 2001). Any other known methods of polypeptide detection are also envisaged

5 in connection with the invention. Optimization of protein detection procedures for diagnosis is well known in the art and described herein below. Specifically, diagnostic assays using the above methods may be carried out essentially as follows: Immunohistochemistry for diagnosis may be carried out essentially as described in Diagnostic Immunohistochemistry, David J., MD Dabbs, Churchill Livingstone, 1<sup>st</sup>

10 Ed, 2002; Quantitative Immunohistochemistry: Theoretical Background and its Application in Biology and Surgical Pathology, Fritz et al., Gustav Fischer, 1992. Western blotting-based diagnosis may be carried out essentially as described in Brys et al., "p53 protein detection by the Western blotting technique in normal and neoplastic specimens of human endometrium", *Cancer Letters* 2000; 148 (197-205);

15 Rochon et al., "Western blot assay for prostate-specific membrane antigen in serum of prostate cancer patients" *Prostate* 1994; 25(4): 219-23; Dalmau et al., "Detection of the anti-Hu antibody in the serum of patients with small cell lung cancer-- a quantitative western blot analysis", *Ann Neurol* 1990; 27(5): 544-52; Joyce et al., "Detection of altered H-ras proteins in human tumors using western blot analysis",

20 *Lab Invest* 1989; 61(2): 212-8. ELISA based diagnosis may be carried out essentially as described in D'ambrosio et al., "An enzyme-linked immunosorbent assay (ELISA) for the detection and quantitation of the tumor marker 1-methylinosine in human urine", *Clin Chim Acta* 1991; 199(2): 119-28; Attalah et al., "A dipstick, dot-ELISA assay for the rapid and early detection of bladder cancer", *Cancer Detect Prev* 1991;

25 15(6): 495-9; Erdile et al., "Whole cell ELISA for detection of tumor antigen expression in tumor samples", *Journal of Immunological Methods* 2001; 258: 47-53. Antibody microarray-based diagnosis may be carried out essentially as described in Huang, "detection of multiple proteins in an antibody-based protein microarray system", *Immunol Methods* 2001 1; 255 (1-2): 1-13. Targeted molecular imaging-based

30 diagnosis may be carried out essentially as described in Thomas, Targeted Molecular Imaging in Oncology, Kim et al (Eds), Springer Verlag, 2001; Shahbazi-Gahruei et al., "In vitro studies of gadolinium-DTPA conjugated with monoclonal antibodies as cancer-specific magnetic resonance imaging contrast agents", *Australas Phys Eng Sci Med* 2002; 25(1): 31-8; Tiefenauer et al., "Antibody-magnetite nanoparticles: in

vitro characterization of a potential tumor-specific contrast agent for magnetic resonance imaging", *Bioconjug Chem* 1993; 4(5): 347-52; Cerdan et al., "Monoclonal antibody-coated magnetite particles as contrast agents in magnetic resonance imaging of tumors", *Magn Reson Med* 1989; 12(2): 151-63. In addition, polypeptides may be detected and a diagnostic assay performed using Mass Spectrometry, essentially as described in Bergquist et al., "peptide mapping of proteins in human body fluids using electrospray ionization fourier transform ion cyclotron resonance mass spectrometry", *Mass Spectrometry Reviews*, 2002; 21:2-15 and Gelpi, "Biomedical and biochemical applications of liquid-chromatography-mass spectrometry", *Journal of Chromatography A*, 1995; 703: 59-80.

An additional embodiment of the diagnostic aspect of the invention provides for a method of diagnosing a cancer in a subject comprising determining, in a sample from the subject, the level of at least one polypeptide-encoding polynucleotide, wherein a higher level of the polynucleotide compared to the level of the polynucleotide in a subject free of cancer is indicative of cancer, and wherein the polynucleotide is selected from the group consisting of human polynucleotides or the human orthologs of mouse polynucleotides listed in Tables 5 and 6, preferably in Table 6, polynucleotides having sequences that differ from these polynucleotides without changing the polypeptide encoded thereby, and homologs thereof having at least 70% homology, preferably at least 80% homology, more preferably at least 90% homology.

The sample may originate from a tissue or a bodily fluid, as described above.

Methods of determining the level of a polynucleotide in a sample are well known in the art and include, *inter alia*: RT-PCR analysis, in-situ hybridization and northern blotting; polynucleotide detection may also be performed by hybridizing a sample with a microarray imprinted with markers. Any other known methods of polynucleotide detection are also envisaged in connection with the invention. Optimization of polynucleotide detection procedures for diagnosis is well known in the art and described herein below. Specifically, diagnostic assays using the above methods are well known in the art (see, for example: Sidransky, "Nucleic Acid-Based methods for the Detection of Cancer", *Science*, 1997; 278: 1054-1058) and may be carried out essentially as follows: RT-PCR for diagnosis may be carried out essentially as described in Bernard & Wittwer, "Real-Time PCR Technology for



Cancer Diagnostics", *Clinical Chemistry* 2002; 48(8): 1178-85; Raj et al., "Utilization of Polymerase Chain Reaction Technology in the Detection of Solid Tumors", *Cancer* 1998; 82(8): 1419-1442; Zippelius & Pantel, "RT-PCR-based detection of occult disseminated tumor cells in peripheral blood and bone marrow of patients with solid tumors. An overview", *Ann NY Acad Sci* 2000; 906:110-23. In-situ hybridization for diagnosis may be carried out essentially as described in "Introduction to Fluorescence In Situ Hybridization: Principles and Clinical Applications", Andreoff & Pinkel (Editors), John Wiley & Sons Inc., 1999; Cheung et al., "Interphase cytogenetic study of endometrial sarcoma by chromosome in situ hybridization, modern Pathology 1996; 9:910-918. Northern blotting for diagnosis may be carried out essentially as described in Trayhum, "Northern blotting", *Proc Nutr Soc* 1996; 55(1B): 583-9; Shifman & Stein, "A reliable and sensitive method for non-radioactive Northern blot analysis of nerve growth factor mRNA from brain tissues", *Journal of Neuroscience Methods* 1995; 59: 205-208; Pacheco et al., "Prognostic significance of the combined expression of matrix metalloproteinase-9, urokinase type plasminogen activator and its receptor in breast cancer as measured by Northern blot analysis", *Int J Biol Markers* 2001; 16(1): 62-8. Polynucleotide microarray-based diagnosis can be carried out essentially as described in Ring & Boss, "Microarrays and molecular markers for tumor classification", *Genome Biol* 2002; 3(5): comment2005; Lacroix et al., "A low-density DNA microarray for analysis of markers in breast cancer", *Int J Biol Markers* 2002; 17(1): 5-23. In addition, polynucleotide microarray hybridization for diagnosis may be carried out essentially as described in the following review concerning micorarrays in the diagnosis of various cancers: Schmidt & Begley, "Cancer diagnosis and microarrays", *The International Journal of Biochemistry and Cell Biology*, 2003; 35: 119-124. Diagnostic assays using tissue microarrays are also possible and may be performed essentially as described in Ginestier et al., "Distinct and complementary information provided by use of tissue and DNA microarrays in the study of breast tumor markers", *Am J Pathol* 2002; 161(4): 1223-33; Fejzo & Slamon, "Frozen tumor tissue microarray technology for analysis of tumor RNA, DNA and proteins", *Am J Pathol* 2001; 159(5): 1645-50.

An example of detection of polynucleotides in bodily fluid is that of "staging" markers, which determine the stage of a cancer by detection of the presence of specific cancer cells in the blood (micrometastases) by RT-PCR of identified cancer-type-specific markers expression on the whole blood RNA (provided these

markers are not normally expressed in blood cells) such detection and diagnosis can be carried out essentially as described in Luke & Kaul, "Detection of Breast Cancer Cells in Blood Using Immunomagnetic Bead Selection and Reverse Transcription-Polymerase Chain Reaction", *Mol Diagn* 1998; 3(3): 149-155; Ghossein et al., "Molecular Detection of Micrometastases and Circulating Tumor Cells in Solid Tumors", *Clinical Cancer Research* 1999; 5: 1950-1960; Mellado et al., "Detection of circulating neoplastic cells by reverse-transcriptase polymerase chain reaction in malignant melanoma: association with clinical stages and prognosis", *J Clin Oncol* 1996; 14(7): 2091-7.

Any of the diagnostic methods as described above can also be used together, simultaneously or not, and can thus provide a stronger diagnostic tool and validate or strengthen the results of a particular diagnosis. For combinations of different diagnostic methods see, *inter alia*: Hoshi et al., "Enzyme-linked immunosorbent assay detection of prostate-specific antigen messenger ribonucleic acid in prostate cancer", *Urology* 1999; 53 (1): 228-235; Zhong-Ping et al., "Quantitation of ERCC-2 Gene Expression in Human Tumor Cell Lines by Reverse Transcription-Polymerase Chain Reaction in Comparison to Northern Blot Analysis", *Analytical Biochemistry* 1997; 244: 50-54; Hatta et al., "Polymerase chain reaction and immunohistochemistry frequently detect occult melanoma cells in regional lymph nodes of melanoma patients", *J Clin Pathol* 1998; 51(8): 597-601.

Any one of the diagnostic methods of the invention as recited above may also be employed to examine the status of a tumor suppressor gene or a biological pathway in which a tumor suppressor gene is involved, or to examine the effectiveness of a modulator of the activity of a tumor suppressor gene, such as a drug. The tumor suppressor gene in question may preferably be any one of p53, Rb1 and PTEN, as well as any other tumor suppressor gene deemed suitable. A list of tumor suppressor genes is provided above.

A preferred embodiment of the prognostic aspect of the invention concerns a method of measuring the responsiveness of a subject to a cancer treatment comprising determining the level of at least one polypeptide in a sample taken from the subject before treatment, and comparing it with the level of said polypeptide in a sample taken from the subject after treatment, a decrease in said level indicating responsiveness of said subject to the cancer treatment, wherein the polypeptide is selected from the group consisting of: polypeptides encoded by the human

polynucleotides or the human orthologs of mouse polynucleotides listed in Table 5 or 6, and homologs of said polypeptides having at least 70% homology, preferably at least 80% homology, more preferably at least 90% homology.

As mentioned herein, the sample may be taken from a bodily fluid, as described above; the level of the polypeptide in the sample can be determined as described above.

In addition, the prognostic aspect of the invention comprises further a method of measuring the responsiveness of a subject to a cancer treatment comprising determining the level of at least one polypeptide-encoding polynucleotide in a sample taken from the subject before treatment, and comparing it with the level of said polynucleotide in a sample taken from the subject after treatment, a decrease in said level indicating responsiveness of said subject to the cancer treatment, wherein the polynucleotide is selected from the group consisting of: human polynucleotides or the human orthologs of mouse polynucleotides listed in Table 5 and 6, preferably in Table 6, polynucleotides having sequences that differ from these polynucleotides without changing the polypeptide encoded thereby, and homologs thereof having at least 70% homology, preferably at least 80% homology, more preferably at least 90% homology.

The sample may originate from a tissue, preferably blood or bone marrow cells, or a bodily fluid, as described above.

The level of the polynucleotide in the sample is determined by the methods disclosed above, preferably by RT-PCR analysis. Any other polynucleotide detection methods disclosed herein may also be employed.

In accordance with the prognostic aspect of the invention, the treatment in conjunction with which the above methods of measuring the responsiveness of a subject to a cancer treatment may be employed include, *inter alia*, radiotherapy or administration of a chemotherapeutic drug such as etoposide, 5-FU (5-fluorouracil), cis-platinum, doxorubicin, a vinca alkaloid, vincristine, vinblastine, vinorelbine, taxol, cyclophosphamide, ifosfamide, chlorambucil, busulfan, mechlorethamine, mitomycin, dacarbazine, carboplatinum, thiotepa, daunorubicin, idarubicin, mitoxantrone, bleomycin, esperamicin A1, dactinomycin, plicamycin, carmustine, lomustine, tauromustine, streptozocin, melphalan, dactinomycin, procarbazine, dexamethasone, prednisone, 2-chlorodeoxyadenosine, cytarabine, docetaxel, fludarabine, gemcitabine, herceptin, hydroxyurea, irinotecan, methotrexate,

oxaliplatin, rituxin, semustine, tomudex and topotecan, and chemotherapeutically active analogs of these drugs.

In a further embodiment of the prognostic aspect of the invention, the methods disclosed herein may also be indicative of the status of a tumor suppressor gene, as described above. Where a tumor suppressor gene or a pathway in which such gene is involved is defective or abnormal, this information may also serve in prognosis of both disease progression and treatment responsiveness of a patient, regardless of whether said treatment is directed to the tumor suppressor in question.

In an additional embodiment, the diagnostic and prognostic methods of the invention may also be carried out essentially as described herein wherein the method comprises determining the level of at least two polypeptides or polypeptide-encoding polynucleotides in a sample taken from a subject. Methods of determining the level of polypeptides and polynucleotides are described above.

Different combinations of polypeptides or polynucleotides of the cancer markers may be employed in different diagnostic or prognostic methods for various cancers.

For bodily fluid sample based diagnosis or prognosis, at least one polypeptide or combination of at least two polypeptides encoded by the human polynucleotide or human orthologs of the polynucleotides, of Table 3 and 5, preferably of Table 5, more preferably of the highlighted genes of Table 5, may be employed as markers.

For tissue sample based diagnosis or prognosis at least one polypeptide or combination of at least two polypeptides encoded by the human polynucleotide or human orthologs of the polynucleotides, of Table 2 and 6, preferably of Table 6, or the polynucleotides themselves may be employed as markers.

For the diagnosis or prognosis of a cancer of a specific tissue, the markers comprise at least one, preferably at least 2, human polypeptides or polynucleotides, or human orthologs of the mouse polypeptides or polynucleotides, or homologs thereof, listed in Table 2 and Table 6. For the tissues breast, placenta/uterus, kidney, bladder, lung, brain, colon, intestine, stomach, liver, pancreas and spleen the above described polypeptides and polynucleotides are listed in Table 2 and Table 6 as follows:

For the diagnosis or prognosis of a cancer of the breast, the markers listed in Table 2 sheet 1 and Table 6, preferably in Table 6 under the heading "breast";

For the diagnosis or prognosis of a cancer of the uterus, the markers listed in Table 2 sheet 2 and Table 6, preferably in Table 6 under the heading "placenta/uterus";

For the diagnosis or prognosis of a cancer of the kidney, the markers listed in Table 2 sheet 3 and Table 6, preferably in Table 6 under the heading "kidney";

For the diagnosis or prognosis of a cancer of the bladder, the markers listed in Table 2 sheet 4 and Table 6, preferably in Table 6 under the heading "bladder";

For the diagnosis or prognosis of a cancer of the lung, the markers listed in Table 2 sheet 5 and Table 6, preferably in Table 6 under the heading "lung";

For the diagnosis or prognosis of a cancer of the brain, the markers listed in Table 2 sheet 6 and Table 6, preferably in Table 6 under the heading "brain";

For the diagnosis or prognosis of a cancer of the colon, the markers listed in Table 2 sheet 7 and Table 6, preferably in Table 6 under the heading "colon";

For the diagnosis or prognosis of a cancer of the intestine, the markers listed in Table 2 sheet 8 and Table 6, preferably in Table 6 under the heading "intestine";

For the diagnosis or prognosis of a cancer of the stomach, the markers listed in Table 2 sheet 9 and Table 6, preferably in Table 6 under the heading "stomach";

For the diagnosis or prognosis of a cancer of the liver, the markers listed in Table 2 sheet 10 and Table 6, preferably in Table 6 under the heading "liver";

For the diagnosis or prognosis of a cancer of the pancreas, the markers listed in Table 2 sheet 11 and Table 6, preferably in Table 6 under the heading "pancreas";

For the diagnosis or prognosis of a cancer of the spleen, the markers listed in Table 2 sheet 12 and Table 6, preferably in Table 6 under the heading "spleen."

The invention further comprises a method of identifying a diagnostic marker for a cancer comprising:

(a) obtaining a first cell from a first cell type of said cancer, said cell comprising a defective tumor suppressor expression;

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- (b) obtaining a second cell of the first cell type, wherein said second cell comprises a wild-type tumor suppressor expression;
- (c) identifying genes having an increased level of expression in the first cell as compared to the second cell; and
- 5 (d) selecting at least one gene of step (c) as a diagnostic marker for a cancer.

In a related aspect, the invention further comprises a method of identifying a tissue-specific diagnostic marker for a cancer comprising a) obtaining a first cell from a second cell type of the cancer, the cell comprising a defective tumor  
10 suppressor expression; b) obtaining a second cell of the second cell type, wherein the second cell comprises a wild-type tumor suppressor expression; c) identifying genes having an increased level of expression in the first cell of the second cell type as compared to the second cell of the second cell type; d) comparing the genes having an increased expression in the first cell type with the genes having an increased  
15 expression in the second cell type; e) identifying genes having an increased expression in the first cell type but not in the second cell type; and f) selecting at least one gene of step (e) as a diagnostic marker of a cancer of the first cell type.

The identification step of both methods (steps (c) or (e) above, respectively) may be performed using a microarray; in addition, the tumor suppressor  
20 in question may be p53, Rb1 and PTEN as well as any other tumor suppressor gene deemed suitable. A list of possible tumor suppressor genes is provided herein.

In certain embodiments, the diagnostic marker is a secreted product of the first cell type. In certain embodiments, the selected gene is not expressed in other tissue irrespective of its status. In other embodiments, the diagnostic marker is a  
25 membrane bound marker that localizes to the cell membrane of the first cell type. In specific embodiments, the tumor suppressor is selected from the group consisting of p53, Rb1, APC; BRCA1; BRCA2; CDH1; p57, p16, CYLD; p300; EXT1; EXT2; MADH4; MAP2K4; MEN1; HNPCC2; MSH2; NF1; NF2; PRKAR1A; PTCH; PTEN; SDHD; SMARCB1; STK11; TSC1; TSC2; VHL and WT1.

30 An additional embodiment of the invention concerns a method for screening for compounds that modulate the activity of a tumor suppressor gene comprising: a) obtaining a cell comprising a defective tumor suppressor expression;

b) measuring the level of expression of a marker of Table 5 or 6 in the cell; c) contacting the cell with a test compound; and d) measuring the expression of the marker of step b) after the contacting step c), wherein a change in the level of expression after the contacting step as compared to the level of expression before the contacting step is indicative of the ability of the compound to modulate the activity of the tumor suppressor gene.

The tumor suppressor in question may be selected from the tumor suppressor group consisting of, *inter alia*, p53, Rb1, APC; BRCA1; BRCA2; CDH1; p57, p16, CYLD; p300; EXT1; EXT2; MADH4; MAP2K4; MEN1; HNPCC2; MSH2; NF1; NF2; PRKAR1A; PTCH; PTEN; SDHD; SMARCB1; STK11; TSC1; TSC2; VHL and WT1. The test compound may be a small chemical molecule. The measuring of steps b) and d) may comprise monitoring the level of mRNA of the marker or the level of the polypeptide of the marker, according to methods well known in the art and described herein. In addition, the change in the level of expression in step d) may be a reduction in the level of expression, in which case compounds identified according to said method may be employed in the treatment of cancer, possibly as anti-cancer drugs.

The term "small chemical molecule" is used interchangeably with "chemical compound", and is understood to refer to chemical moieties of any particular type which are not necessarily, but may be, naturally occurring and typically have a molecular weight of less than 2000 daltons, more preferably less than 1000 daltons.

Another aspect of the invention provides a microarray composition for measuring tissue-specific gene expression comprising at least 4 polynucleotides from tables 5 and 6. The invention further contemplates a method of diagnosing a cancer comprising contacting a cell sample nucleic acid with a microarray described herein under conditions suitable for hybridization; providing hybridization conditions suitable for hybrid formation between said cell sample nucleic acid and a polynucleotide of said microarray; detecting said hybridization; and diagnosing a cancer based on the results of detecting said hybridization.

Further in this aspect, an antibody microarray is provided. Said microarray comprises at least 4 antibodies directed against polypeptides corresponding to the polynucleotides given in Tables 5 and 6. The invention further

contemplates a method of diagnosing a cancer comprising contacting a bodily fluid sample with the antibody microarray described herein, and detecting hybridization between the antibodies present on the array and at least one polypeptide present in the bodily fluid, the results of said detection enabling a diagnosis or a prognosis of a cancer.

The invention further contemplates a vector comprising a polynucleotide having a sequence of a tissue specific tumor marker identified according to the invention. Also contemplated is a cell transformed or transfected with such a vector.

Another aspect of the invention is directed to a method of treating cancer in a patient, wherein said treatment is effected through the decrease in expression of a tumor marker gene. In preferred embodiments, a polynucleotide is administered to cancer cells of a patient. The polynucleotide comprises an antisense sequence of said tissue-specific tumor marker in those embodiments where the tissue-specific tumor marker is up-regulated as a result of loss of function of the tumor suppressor, whereas the polynucleotide comprises a sense coding sequence of said tissue-specific tumor marker in those embodiments where the tissue specific marker is down-regulated as a result of loss of function of the tumor suppressor. In specific embodiments, the cancer cells of the patient harbor a mutant tumor suppressor gene selected from the group consisting of p53, Rb1, APC; BRCA1; BRCA2; CDH1; p57, p16, CYLD; p300; EXT1; EXT2; MADH4; MAP2K4; MEN1; HNPCC2; MSH2; NF1; NF2; PRKAR1A; PTCH; PTEN; SDHD; SMARCB1; STK11; TSC1; TSC2; VHL and WT1.

By "homolog/homology", as related to polynucleotides and polypeptides and used herein, is meant at least about 70%, preferably at least about 75% homology, advantageously at least about 80% homology, more advantageously at least about 90% homology, even more advantageously at least about 95%, e.g., at least about 97%, about 98%, about 99% or even about 100% homology. The invention also comprehends that these polynucleotides and polypeptides can be used in the same fashion as the herein or aforementioned polynucleotides and polypeptides.

Alternatively or additionally, "homology", with respect to sequences, can refer to the number of positions with identical nucleotides or amino acid residues, divided by the number of nucleotides or amino acid residues in the shorter of the two sequences, wherein alignment of the two sequences can be determined in accordance



with the Wilbur and Lipman algorithm ((1983) Proc. Natl. Acad. Sci. USA 80:726), for instance, using a window size of 20 nucleotides, a word length of 4 nucleotides, and a gap penalty of 4, and computer-assisted analysis and interpretation of the sequence data, including alignment can be conveniently performed using commercially available programs (e.g., Intelligenetics™ Suite, Intelligenetics Inc., CA). When RNA sequences are said to be similar, or to have a degree of sequence identity or homology with DNA sequences, thymidine (T) in the DNA sequence is considered equal to uracil (U) in the RNA sequence. RNA sequences within the scope of the invention can be derived from DNA sequences or their complements, by substituting thymidine (T) in the DNA sequence with uracil (U).

Additionally or alternatively, amino acid sequence similarity or homology can be determined, for instance, using the BlastP program (Altschul *et al.*, Nucl. Acids Res. 25:3389-3402) and available at NCBI. The following references provide algorithms for comparing the relative identity or homology of amino acid residues of two polypeptides, and additionally, or alternatively, with respect to the foregoing, the teachings in these references can be used for determining percent homology: Smith *et al.*, (1981) Adv. Appl. Math. 2:482-489; Smith *et al.*, (1983) Nucl. Acids Res. 11:2205-2220; Devereux *et al.*, (1984) Nucl. Acids Res. 12:387-395; Feng *et al.*, (1987) J. Molec. Evol. 25:351-360; Higgins *et al.*, (1989) CABIOS 5:151-153; and Thompson *et al.*, (1994) Nucl. Acids Res. 22:4673-4680.

The term "polynucleotide" refers to any molecule which comprises two or more of the bases guanine, cytosine, thymine, adenine, uracil or inosine, inter alia, or chemical analogs thereof, includes "oligonucleotides" and encompasses "nucleic acids". Preferably, a polynucleotide has from about 75 to 10,000 nucleotides, more preferably from about 100 to 3,500 nucleotides. An oligonucleotide refers generally to a chain of nucleotides extending from 2-75 nucleotides.

By the term "polypeptide" is meant a molecule composed of amino acids and the term includes peptides, polypeptides, proteins and peptidomimetics; dominant polypeptide fragments are also considered to be polypeptides.

The term "amino acid" refers to any one of the 20 naturally occurring amino acids, and also amino acids which have been chemically modified or synthetic amino acids.

The invention provides methods for the identification of marker gene targets for both diagnostic and therapeutic applications in any given cancer type. In

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certain embodiments, these methods use a combination of recently developed powerful functional gene cloning methodologies with cDNA array-based gene expression profiling and rationally designed experimental models. Diagnostic and therapeutic value of the identified genes may then be evaluated using specific inhibitors and antibodies according to methods well known to those of skill in the art.

By identifying those genes that are specifically upregulated (or indeed downregulated) in cancer cells as a result of tumor suppressor regulation, the invention provides markers of advanced stages of cancer. More specifically, the invention relates to identifying potential targets of tumor suppressor regulation associated with early and advanced stages of the disease by performing micro-array hybridization and analyses using model cancer cell line(s) or primary normal cell cultures that retain wild-type tumor suppressor activity and engineering a variant of such a cell line or primary cells in which the tumor suppressor is inactivated. Alternatively, the tissue pairs for comparison will be normal animal tissues and the same cancer-free tissues from genetically modified animals in which a tumor suppressor gene of interest was knocked out.

The methods of the invention generally provide a systematic approach for the search of cancer markers or targets for therapeutic intervention among the genes normally under negative control of tumor suppressor proteins. Many such genes are transcriptionally activated in tissues following the wild-type activity loss of the most common tumor suppressor genes, such as p53, PTEN, RB, and p16/p19 and this regulation is conserved in normal and tumor cells from the same origin. The methods of the invention may be performed by comparing gene expression profiles in the isogenic pairs of cell lines or tissues differing in their tumor suppressor gene status or tissue pairs derived from normal and genetically modified mice, with inactivated tumor suppressors, i.e. p53 <sup>-/-</sup> mice, p16/p19<sup>-/-</sup> mice, and mice with targeted expression of, e.g., SV40 large T antigen that simultaneously inactivates both RB and p53 function (TRAMP mice).

In an exemplary model for the invention, the inventors created an isogenic pair of LNCaP prostate tumor cell lines differing in their p53 status and applied cDNA microarray analysis to identify differentially expressed genes. These investigations revealed that the baseline expression of several known tumor markers is significantly elevated in LNCaP cells that lack functional p53 protein compared to the same cells that express wt p53. These genes include e.g., COX2, tumor-specific

heparin-binding growth factor midkine (which possesses angiogenic and anti-apoptotic properties) (Ikematsu *et al.*, *Br J Cancer*, 83(6):701-706 (2000), tumor tissue associated hyaluronan receptor CD44 and PSA (prostate specific antigen). COX2 inhibitors are currently in clinical trials against prostate cancer. Midkine was

5 immunohistochemically shown to be expressed in 86.3% of prostate cancer specimens examined, with metastatic lesions generally showing higher expression than the corresponding primaries; normal prostate tissues were negative or showed only weak staining. Midkine was also detected in 12 of 15 latent cancers (80%) and in 12 of 16 cases of PIN (75%) (Konishi *et al.*, *Oncology*, 57(3):253-257 (1999).

10 PSA is the major prostate cancer diagnostic marker currently used commercially. In the invention, it was shown that the PSA promoter is directly suppressed by wt p53, thus PSA up-regulation in prostate cancer is indicative of the loss of wt p53 function. The list of genes the expression of which was changed following wt p53 suppression in LNCaP cells is attached in Table 1. Having

15 determined that it is thus possible to identify the differential expression of genes that are regulated by suppression of the wild-type tumor suppressor, the inventors further demonstrate large-scale microarray-based comparison of gene-expression profiles in the tissue pairs derived from normal and p53-/- mice.

Poly A RNA was extracted from spleen, pancreas, liver, stomach,

20 intestine, colon, lung, brain, bladder, kidney, placenta/uterus and mammary glands of normal and p53-deficient mice and used for fluorescently-labeled probes for microarray hybridizations. The differential (against common control) gene expression levels were normalized between p53-/- tissues and their corresponding normal counterparts. (Table 2). These data were then sorted according to their expression

25 levels in one particular tissue from maximally up-regulated genes to maximally down-regulated genes, thereby identifying genes with maximal differential tissue-specific expression in p53-deficient mice.

Of the identified genes, the tumor makers will be those that are found to be up-regulated in p53-/-tissues. Table 3 lists such genes; the table combines the

30 p53-dependent differential expression data with the tissue specificity of gene expression data. Differential expression of the genes may be determined using any technique well known to those of skill in the art. Such techniques include determining differential expression using cDNA or oligonucleotide microarrays as described herein below, as well as differential display techniques well known to those

of skill in the art. Gene subtraction techniques also may be used. Also contemplated for determining differential expression of genes is SAGE (Velculescu *et al.*, *Science*, 270:484-487 (1995); Zhang *et al.*, *Science*, 276:1268-1272 (1997).

For effective selection of cancer diagnostic markers, the following  
5 criteria were applied:

(1) genes that are up-regulated in a certain p53<sup>-/-</sup> tissue and are normally expressed predominantly in that tissue are useful for diagnosis both in tissues and in bodily fluids. Table 5 is derived from Table 3 and contains a list of the preferred genes which can serve as markers of this type (the highlighted genes are  
10 highly preferred).

(2) genes that are normally expressed at certain levels in one or several tissues but are up-regulated in one or numerous p53<sup>-/-</sup> tissues as compared to the same tissue having normal p53 status are useful for diagnosis primarily in tissues. Table 6 is derived from Table 2 and contains a list of the preferred markers of this  
15 type, sorted according to the tissue in which they are preferred for diagnosis. Both tables are prioritized, so that, for example, under the heading "pancreas" in Table 6 or in sheet 11 of Table 2, the first marker listed, pancreatitis associated protein, is the most preferred marker for pancreatic cancer.

Table 3 contains 445 genes identified as being up-regulated in p53<sup>-/-</sup>  
20 tissues, which can serve as tissue specific cancer markers and for bodily-fluid cancer diagnosis, depending on their level of expression in normal tissues, which tissues they are normally expressed in, and whether they are secreted.

The genes identified according to the invention will prove useful in diagnostic and prognostic application as well as act as drug targets for therapeutic  
25 intervention of the diseased state. Negative regulation by tumor suppressor genes and tissue specificity of expression are two essential characteristics of prospective tumor markers/drug targets. However, in order to be suitable for diagnostic assays, the gene products ideally, but not necessarily, also need to be secreted into blood, urine, saliva or any other accessible body fluids for detection. Alternatively, the gene products are  
30 such that they are expressed at the cell surface and are therefore amenable to detection using ordinary techniques known to those of skill in the art, *e.g.*, detection of cell surface expression of the gene products using antibodies or ligand/receptor interactions. Membrane-bound and cytosolic RNA may be distinguished based on the fact that mRNA of genes, encoding secreted or membrane proteins is bound to

membrane-associated polysomes and may be separated from other mRNAs by sedimentation equilibrium or sedimentation velocity (Diehn *et al.*, *Nat. Genet.*, 25:58-62, 2000). RNA from membrane or cytosolic fraction of cells will be isolated using standard protocol and used for synthesis of fluorescently labeled probe from each fraction. Isolation of membrane-bound polysomes from cell lines preferably is carried out according to published protocol (Diehn *et al.*, *Nat. Genet.*, 25:58-62 (2000). See also U.S. Patent No. 6,403,316.

In summary, the inventors defined genes characterized in regard to tissue-specificity of the normal expression of these genes and induction/reduction in various p53-deficient tissues. The above-articulated method, while exemplified in terms of p53 regulation, may be performed with any tumor suppressor known to those of skill in the art to identify tissue-specific markers of cancers. In addition to p53, tumor suppressors such as Rb1, APC; BRCA1; BRCA2; CDH1; p57, p16, CYLD; p300; EXT1; EXT2; MADH4; MAP2K4; MEN1; HNPCC2; MSH2; NF1; NF2; PRKAR1A; PTCH; PTEN; SDHD; SMARCB1; STK11; TSC1; TSC2; VHL; WT1, are exemplary tumor suppressors that may be employed to identify tissue-specific tumor marker genes according to the invention. This is by no means an exhaustive list and those of skill in the art will be aware of other tumor suppressors that may be used in the methods herein. Those of skill in the art will readily be able to obtain the sequences for these tumor suppressor genes from Genbank.

## I. Diagnostic Methods of Using Identified Markers

In the genetic diagnostic applications of the invention, one of skill in the art would detect variations in the expression of one or more of the tissue-specific tumor markers. This may comprise determining the mRNA level of the gene(s) or determining specific alterations in the expressed gene product(s). The cancers that may be diagnosed according to the invention include cancers of the brain (glioblastomas, medulloblastoma, astrocytoma, oligodendroglioma, ependymomas), lung, liver, spleen, kidney, pancreas, intestine, blood cells, lymph node, colon, breast, endometrium, stomach, prostate, testicle, ovary, skin, head or neck, esophagus, bone marrow, blood or other tissue.

The biological sample can be any tissue or fluid. Various embodiments include cells of the skin, muscle, facia, brain, prostate, breast, endometrium, lung,

head or neck, pancreas, small intestine, blood cells, liver, testes, ovaries, colon, skin, stomach, esophagus, spleen, lymph node, bone marrow or kidney. Other embodiments include fluid samples such as peripheral blood, lymph fluid, ascites, serous fluid, pleural effusion, sputum, cerebrospinal fluid, lacrimal fluid, synovial fluid, saliva, stool or urine.

Nucleic acids can be isolated from cells contained in the biological sample, according to standard methodologies (Sambrook *et al.*, 1989). The nucleic acid may be whole RNA. It may be used for Northern blotting analysis or may be converted to a complementary DNA (cDNA). In one embodiment, the RNA is whole cell RNA; in another, it is poly-A RNA. cDNA may be used for preparation of probes for microarray hybridization or may be amplified in PCR reaction (RT-PCR).

In situ hybridization using a labeled nucleic acid probe is performed essentially as known in the art and incorporated herein by reference.

Depending on the format, the specific nucleic acid of interest is identified in the sample directly using amplification or by hybridization to a labeled (radioactively or fluorescently) nucleic acid probe. Next, the identified amplified product is detected. In certain applications, the detection may be performed by visual means (e.g., ethidium bromide staining of a gel). Alternatively, the detection may involve indirect identification of the product via chemiluminescence, radioactive scintigraphy of radiolabel or fluorescent label or even via a system using electrical or thermal impulse signals (Affymax Technology; Bellus, 1994).

#### A. Microarray Analyses

In certain preferred embodiments, DNA-based arrays provide a convenient way to explore the expression of a single polymorphic gene or a large number of genes for a variety of applications. The tissue-specific tumor marker nucleic acids identified by the invention may be presented in a DNA microarray for the analysis and expression of these genes in various cancer cell types. Microarray chips are well known to those of skill in the art (see, e.g., U.S. Patent Nos. 6,308,170; 6,183,698; 6,306,643; 6,297,018; 6,287,850; 6,291,183, each incorporated herein by reference). These are exemplary patents that disclose nucleic acid microarrays and those of skill in the art are aware of numerous other methods and compositions for producing microarrays.

In addition, protein and antibody microarrays are well known in the art (see, for example: Ekins R.P., *J Pharm Biomed Anal* 1989. 7: 155; Ekins R.P. and Chu F.W., *Clin Chem* 1991. 37: 1955; Ekins R.P. and Chu F.W., *Trends in Biotechnology*, 1999, 17, 217-218). Antibody microarrays directed against a combination of the diagnostic markers disclosed herein will be very useful for the diagnosis of cancer markers in bodily fluids.

The invention provides for a composition comprising a plurality of polynucleotides identified according to the methods of the invention. As used herein, the term "polynucleotide probe" refers to any nucleic acid sequences identified according to the invention as a marker for a given cancer. Preferably, the polynucleotide fragment is at least 9 nucleotides; more preferably, it is at least 20 nucleotides. Such a composition can be employed for the diagnosis and treatment of neoplastic disorder.

The composition is particularly useful as hybridizable array elements in a microarray for monitoring the expression of a plurality of target polynucleotides. The microarray comprises a substrate and the hybridizable array elements. The microarray is used, for example, in the diagnosis and treatment of a cancer.

The term "microarray" refers to an ordered arrangement of hybridizable array elements. The array elements are arranged so that there are preferably at least two or more different array elements, more preferably at least 100 array elements, and most preferably at least 1,000 array elements, on a 1 cm<sup>2</sup> substrate surface. The hybridization signal from each of the array elements is individually distinguishable. In a preferred embodiment, the array elements comprise polynucleotide probes. In another preferred embodiment, the array elements comprise antibodies.

The term "probe" refers to a polynucleotide sequence capable of hybridizing with a target sequence to form a polynucleotide probe/target complex. A "target polynucleotide" refers to a chain of nucleotides to which a polynucleotide probe can hybridize by base pairing. In some instances, the sequences will be complementary (no mismatches) when aligned. In other instances, there may be up to a 10% mismatch.

Alternatively, the term "probe" may refer to a polypeptide probe that can hybridize to an antibody.

A "plurality" refers preferably to a group of at least 15 or more members, more preferably to a group of at least about 100, and even more preferably to a group of at least about 1,000, members. The maximum number of members is unlimited, but is at least about 100,000 members.

5 The term "gene" or "genes" refers to a polynucleotide sequence(s) of a gene, which may be the partial or complete sequence of the gene and may comprise regulatory region(s), untranslated region(s), or coding regions.

The polynucleotide or antibody microarray can be used for large-scale genetic or gene expression analysis of a large number of target polynucleotides or polypeptides respectively. The microarray can also be used in the diagnosis of diseases and in the monitoring of treatments. Further, the microarray can be employed to investigate an individual's predisposition to a disease. Furthermore, the microarray can be employed to investigate cellular responses to infection, drug treatment, and the like.

15 When the composition of the invention is employed as hybridizable array elements in a microarray, the array elements are organized in an ordered fashion so that each element is present at a distinguishable, and preferably specified, location on the substrate. In the preferred embodiments, because the array elements are at specified locations on the substrate, the hybridization patterns and intensities (which together create a unique expression profile) can be interpreted in terms of expression levels of particular genes and can be correlated with a particular disease or condition or treatment.

The composition comprising a plurality of polynucleotide probes can also be used to purify a subpopulation of mRNAs, cDNAs, genomic fragments and the like, in a sample. Typically, samples will include target polynucleotides of interest and other nucleic acids which may enhance the hybridization background; therefore, it may be advantageous to remove these nucleic acids from the sample. One method for removing the additional nucleic acids is by hybridizing the sample containing target polynucleotides with immobilized polynucleotide probes under hybridizing conditions. Those nucleic acids that do not hybridize to the polynucleotide probes are removed and may be subjected to analysis or discarded. At a later point, the immobilized target polynucleotide probes can be released in the form of purified target polynucleotides.

# 1. Microarray Production



The nucleic acid probes can be genomic DNA or cDNA or mRNA, or any RNA-like or DNA-like material, such as peptide nucleic acids, branched DNAs, and the like. The probes can be sense or antisense polynucleotide probes. Where target polynucleotides are double-stranded, the probes may be either sense or antisense strands. Where the target polynucleotides are single-stranded, the probes are complementary single strands.

In one embodiment, the probes are cDNAs. The size of the DNA sequence of interest may vary and is preferably from 100 to 10,000 nucleotides, more preferably from 150 to 3,500 nucleotides.

The probes can be prepared by a variety of synthetic or enzymatic schemes, which are well known in the art. The probes can be synthesized, in whole or in part, using chemical methods well known in the art (Caruthers *et al.*, *Nucleic Acids Res., Symp. Ser.*, 215-233 (1980). Alternatively, the probes can be generated, in whole or in part, enzymatically.

Nucleotide analogs can be incorporated into the probes by methods well known in the art. The only requirement is that the incorporated nucleotide analog must serve to base pair with target polynucleotide sequences. For example, certain guanine nucleotides can be substituted with hypoxanthine, which base pairs with cytosine residues. However, these base pairs are less stable than those between guanine and cytosine. Alternatively, adenine nucleotides can be substituted with 2,6-diaminopurine, which can form stronger base pairs than those between adenine and thymidine.

Additionally, the probes can include nucleotides that have been derivatized chemically or enzymatically. Typical chemical modifications include derivatization with acyl, alkyl, aryl or amino groups.

The polynucleotide probes can be immobilized on a substrate. Preferred substrates are any suitable rigid or semi-rigid support including membranes, filters, chips, slides, wafers, fibers, magnetic or nonmagnetic beads, gels, tubing, plates, polymers, microparticles and capillaries. The substrate can have a variety of surface forms, such as wells, trenches, pins, channels and pores, to which the polynucleotide probes are bound. Preferably, the substrates are optically transparent.

Complementary DNA (cDNA) can be arranged and then immobilized on a substrate. The probes can be immobilized by covalent means such as by chemical bonding procedures or UV. In one such method, a cDNA is bound to a glass surface

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which has been modified to contain epoxide or aldehyde groups. In another case, a cDNA probe is placed on a polylysine coated surface and then UV cross-linked (Shalon *et al.*, PCT publication WO95/35505, herein incorporated by reference). In yet another method, a DNA is actively transported from a solution to a given position  
5 on a substrate by electrical means (Heller *et al.*, U.S. Pat. No. 5,605,662). Alternatively, individual DNA clones can be gridded on a filter. Cells are lysed, proteins and cellular components degraded, and the DNA coupled to the filter by UV cross-linking.

Furthermore, the probes do not have to be directly bound to the  
10 substrate, but rather can be bound to the substrate through a linker group. The linker groups are typically about 6 to 50 atoms long to provide exposure to the attached probe. Preferred linker groups include ethylene glycol oligomers, diamines, diacids and the like. Reactive groups on the substrate surface react with one of the terminal portions of the linker to bind the linker to the substrate. The other terminal portion of  
15 the linker is then functionalized for binding the probe.

The probes can be attached to a substrate by dispensing reagents for probe synthesis on the substrate surface or by dispensing preformed DNA fragments or clones on the substrate surface. Typical dispensers include a micropipette delivering solution to the substrate with a robotic system to control the position of the  
20 micropipette with respect to the substrate. There can be a multiplicity of dispensers so that reagents can be delivered to the reaction regions simultaneously.

Alternatively, as mentioned above, antibody microarrays can be produced. The production of such microarrays is essentially as described in Schweitzer & Kingsmore, "Measuring proteins on microarrays", *Curr Opin*  
25 *Biotechnol* 2002; 13(1): 14-9; Avseenko *et al.*, "Immobilization of proteins in immunochemical microarrays fabricated by electrospray deposition", *Anal Chem* 2001 15; 73(24): 6047-52; Huang, "Detection of multiple proteins in an antibody-based protein microarray system, *Immunol Methods* 2001 1; 255 (1-2): 1-13. In general, protein microarrays may be produced essentially as described in Schena *et al.*, Parallel human genome analysis: Microarray-based expression monitoring of 1000  
30 genes. *Proc. Natl. Sci. USA* (1996) 93, 10614-10619; U.S. Patent Nos. 6,291,170 and 5,807,522 (see above); US patent No. 6,037,186 (Stimpson, inventor) "Parallel production of high density arrays"; PCT publications WO 99/13313 (Genovations Inc [US], applicant) "Method of making high density arrays"; WO 02/05945 (Max-

Delbruck-center for molecular medicine [Germany], applicant) "Method for producing microarray chips with nucleic acids, proteins or other test substrates".

## 2. Sample Preparation for Genetic Analysis

In order to conduct sample analysis, a sample containing target  
5 polynucleotides or polypeptides is provided. The samples can be any sample containing target polynucleotides or polypeptides and obtained from any bodily fluid (blood, sperm, urine, saliva, phlegm, gastric juices, etc. as described herein), cultured cells, biopsies, or other tissue preparations. The samples being analyzed using the microarrays will likely be samples from individuals suspected of suffering from a  
10 given cancer. In one embodiment, the microarrays used are those that contain tumor markers specific for that cancer or antibodies against those markers.

DNA or RNA can be isolated from the sample according to any of a number of methods well known to those of skill in the art. For example, methods of purification of nucleic acids are described in Tijssen Laboratory Techniques in  
15 Biochemistry and Molecular Biology: Hybridization With Nucleic Acid Probes, Part I. Theory and Nucleic Acid Preparation, Elsevier, New York N.Y. 1993. In one case, total RNA is isolated using the TRIZOL reagent (Life Technologies, Gaithersburg Md.), and mRNA is isolated using oligo d(T) column chromatography or glass beads. Alternatively, when target polynucleotides are derived from an mRNA, the target  
20 polynucleotides can be a cDNA reverse-transcribed from an mRNA, an RNA transcribed from that cDNA, a DNA amplified from that cDNA, an RNA transcribed from the amplified DNA, and the like. When the target polynucleotide is derived from DNA, the target polynucleotide can be DNA amplified from DNA or RNA reverse transcribed from DNA. In yet another alternative, the targets are target  
25 polynucleotides prepared by more than one method.

When target polynucleotides are amplified, it is desirable to amplify the nucleic acid sample and maintain the relative abundances of the original sample, including low abundance transcripts. Total mRNA can be amplified by reverse transcription using a reverse transcriptase and a primer consisting of oligo d(T) and a  
30 sequence encoding the phage T7 promoter to provide a single-stranded DNA template. The second DNA strand is polymerized using a DNA polymerase and a RNase which assists in breaking up the DNA/RNA hybrid. After synthesis of the double-stranded DNA, T7 RNA polymerase can be added, and RNA transcribed from

the second DNA strand template (Van Gelder *et al.* U.S. Pat. No. 5,545,522). RNA can be amplified *in vitro*, *in situ* or *in vivo* (See Eberwine, U.S. Pat. No. 5,514,545).

Quantitation controls may be included within the sample to assure that amplification and labeling procedures do not change the true distribution of target polynucleotides in a sample. For this purpose, a sample is spiked with a known amount of a control target polynucleotide and the composition of probes includes reference probes which specifically hybridize with the control target polynucleotides. After hybridization and processing, the hybridization signals obtained should accurately the amounts of control target polynucleotide added to the sample.

Prior to hybridization, it may be desirable to fragment the nucleic acid target polynucleotides. Fragmentation improves hybridization by minimizing secondary structure and cross-hybridization to other nucleic acid target polynucleotides in the sample or noncomplementary polynucleotide probes. Fragmentation can be performed by mechanical or chemical means.

Antibodies against the relevant cancer marker polypeptides and appropriate for attachment to an antibody microarray can be prepared according to methods known in the art (Coligan *et al.* Unit 9, Current Protocols in Immunology, Wiley Interscience, 1994; Harlow and Lane, Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory, New York (1988). Additional information regarding all types of antibodies, including humanized antibodies, human antibodies and antibody fragments can be found in WO 01/05998).

Polypeptides can be prepared for hybridization to an antibody microarray from a sample, such as a bodily fluid sample, according to methods known in the art. It may be desirable to purify the proteins from the sample or alternatively, to remove certain impurities which may be present in the sample and interfere with hybridization. Protein purification is practiced as is known in the art as described in, for example, Marshak *et al.*, "Strategies for Protein Purification and Characterization. A laboratory course manual." CSHL Press (1996).

The target polynucleotides or polypeptides may be labeled with one or more labeling moieties to allow for detection of hybridized probe/target complexes. The labeling moieties can include compositions that can be detected by spectroscopic, photochemical, biochemical, bioelectronic, immunochemical, electrical, optical or chemical means. The labeling moieties include radioisotopes, such as  $^3\text{H}$ ,  $^{14}\text{C}$ ,  $^{32}\text{P}$ ,  $^{33}\text{P}$  or  $^{35}\text{S}$ , chemiluminescent compounds, labeled binding proteins, heavy metal atoms,

spectroscopic markers, such as fluorescent markers and dyes, magnetic labels, linked enzymes, mass spectrometry tags, spin labels, electron transfer donors and acceptors, and the like.

Exemplary dyes include quinoline dyes, triarylmethane dyes, phthaleins, azo dyes, cyanine dyes, and the like. Preferably, fluorescent markers absorb light above about 300 nm, preferably above 400 nm, and usually emit light at wavelengths at least greater than 10 nm above the wavelength of the light absorbed. Preferred fluorescent markers include fluorescein, phycoerythrin, rhodamine, lissamine, and C3 and C5 available from Amersham Pharmacia Biotech (Piscataway N.J.).

Nucleic acid labeling can be carried out during an amplification reaction, such as polymerase chain reactions and *in vitro* transcription reactions, or by nick translation or 5' or 3'-end-labeling reactions. When the label may be incorporated after or without an amplification step, the label is incorporated by using terminal transferase or by phosphorylating the 5' end of the target polynucleotide using, e.g., a kinase and then incubating overnight with a labeled oligonucleotide in the presence of T4 RNA ligase. Alternatively, the labeling moiety can be incorporated after hybridization once a probe/target complex has formed.

Polypeptide labeling can be conducted using a variety of techniques well known in the art, and the choice of the technique(s) can be tailored to the polypeptide in question according to criteria known to one of skill in the art. Specifically, polypeptides can be fluorescently labeled with compounds such as FITC or rhodamin, essentially as described in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, New York (1988), in particular pages 353-356, or with other fluorescent compounds such as nile red or 2-methoxy-2,4-diphenyl-3(2H)furanone (Daban: *Electrophoresis* 2001; 22(5): 874-80). Polypeptides can also be labeled with a detectable protein such as GFP (detection based on fluorescence) or the vitamin biotin (detection with streptavidin). Polypeptides can also be radioactively labeled with the isotope S<sup>35</sup>. Additional methods are widely known in the art.

### 3. Use of Gene Sequences for Diagnostic Purposes

In certain embodiments, the tissue-specific tumor markers identified herein may be used for the diagnosis of advanced stages of cancer in the given tissue for which the markers are specific. The polynucleotide sequences encoding the tissue specific tumor marker or the polypeptide encoded thereby, where appropriate, may be

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used in in-situ hybridization or RT-PCR assays of fluids or tissues from biopsies to detect abnormal gene expression. Such methods may be qualitative or quantitative in nature and may include Southern or Northern analysis, dot blot or other membrane-based technologies; PCR technologies; chip based technologies (for nucleic acid detection) and dip stick, pin, ELISA and protein-chip technologies (for the detection of polypeptides). All of these techniques are well known in the art and are the basis of many commercially available diagnostic kits.

In addition, such assays may be useful in evaluating the efficacy of a particular therapeutic treatment regime in animal studies, in clinical trials, or in monitoring the treatment of an individual patient. Such monitoring may generally employ a combination of body fluids or cell extracts taken from normal subjects, either animal or human, under conditions suitable for hybridization or amplification. Standard hybridization may be quantified by comparing the values obtained for normal subjects with a dilution series of a tissue-specific tumor marker gene product run in the same experiment where a known amount of purified gene product is used. Standard values obtained from normal samples may be compared with values obtained from samples from cachectic subjects affected by abnormal gene expression in tumor cells. Deviation between standard and subject values establishes the presence of disease.

Generally, the tissue-specific tumor markers are chosen based on the specificity of their expression in tumors as well as on the high correlation of the reactivity of corresponding antibodies with tumor specimens in ELISA and tissue arrays may be used for development of serological screening procedure. For example, in the context of prostate-specific tumor markers, a large scale analysis of serum and sperm samples obtained from normal donors of different age (before and after 60), patients with different grades and types of prostate carcinoma, androgen dependent and androgen independent, with local, recurrent and metastatic disease, patients with tumors of other than prostate origin, as well as patients with noncancerous diseases of prostate may be tested by ELISA on the presence and concentration of the potential candidate polypeptide(s). Then statistical analyses may be performed to evaluate whether the prostate samples express candidate(s) at different levels based on different parameters (histopathological type, Gleason score, tumor size, disease or PSA recurrence).

Once disease is established, a therapeutic agent is administered; and a treatment profile is generated. Such assays may be repeated on a regular basis to evaluate whether the values in the profile progress toward or return to the normal or standard pattern. Successive treatment profiles may be used to show the efficacy of treatment over a period of several days or several months.

PCR as described in U.S. Patent Nos. 4,683,195 and 4,965,188 provides additional uses for oligonucleotides specific for the tissue-specific tumor marker genes. Such oligomers are generally chemically synthesized, but they may be generated enzymatically or produced from a recombinant source as described herein above. Oligomers generally comprise two nucleotide sequences, one with sense orientation and one with antisense orientation, employed under optimized conditions for identification of a specific gene or condition. The same two oligomers, nested sets of oligomers, or even a degenerate pool of oligomers may be employed under less stringent conditions for detection and/or quantitation of closely related DNA or RNA sequences. Methods of performing RT-PCR are standard in the art and the method may be carried out using commercially available kits.

Additionally, methods to quantitate the expression of a particular molecule include radiolabeling (Melby *et al.*, *J Immunol Methods*, 159: 235-244 (1993) or biotinylating (Duplaa *et al.*, *Anal Biochem*, 229-236 (1993) nucleotides, coamplification of a control nucleic acid, and standard curves onto which the experimental results are interpolated. Quantitation of multiple samples may be speeded up by running the assay in an ELISA-like format where the oligomer of interest is presented in various dilutions and a spectrophotometric or colorimetric response gives rapid quantitation. For example, the presence of abnormal levels of a tissue-specific tumor marker in extracts of biopsied tissues will be indicative of the onset of a cancer. A definitive diagnosis of this type may allow health professionals to begin aggressive treatment and prevent further worsening of the condition. Similarly, further assays can be used to monitor the progress of a patient during treatment.

#### 4. Hybridization and Detection in Microarrays

Hybridization causes a denatured probe and a denatured complementary target to form a stable nucleic acid duplex through base pairing. Hybridization methods are well known to those skilled in the art (See, e.g., Ausubel, Short Protocols in Molecular Biology, John Wiley & Sons, New York N.Y., units 2.8-2.11, 3.18-3.19 and 4-6-4.9, 1997). Conditions can be selected for hybridization

where an exactly complementary target and probes can hybridize, i.e., each base pair must interact with its complementary base pair. Alternatively, conditions can be selected where a target and probes have mismatches but are still able to hybridize. Suitable conditions can be selected, for example, by varying the concentrations of salt  
5 in the prehybridization, hybridization and wash solutions, by varying the hybridization and wash temperatures, or by varying the polarity of the prehybridization, hybridization or wash solutions.

Hybridization can be performed at low stringency with buffers, such as 6 x SSPE with 0.005% Triton X-100 at 37°C, which permits hybridization between  
10 target and probes that contain some mismatches to form target polynucleotide/probe complexes. Subsequent washes are performed at higher stringency with buffers, such as 0.5 x SSPE with 0.005% Triton X-100 at 50°C, to retain hybridization of only those target/probe complexes that contain exactly complementary sequences. Alternatively, hybridization can be performed with buffers, such as 5 x SSC/0.2% SDS at 60°C and  
15 washes are performed in 2 x SSC/0.2% SDS and then in 0.1x SSC. Background signals can be reduced by the use of detergent, such as sodium dodecyl sulfate, Sarcosyl or Triton X-100, or a blocking agent, such as salmon sperm DNA.

After hybridization, the microarray is washed to remove nonhybridized nucleic acids, and complex formation between the hybridizable array elements and the  
20 target polynucleotides is detected. Methods for detecting complex formation are well known to those skilled in the art. In a preferred embodiment, the target polynucleotides are labeled with a fluorescent label, and measurement of levels and patterns of fluorescence indicative of complex formation is accomplished by fluorescence microscopy, preferably confocal fluorescence microscopy. An argon ion  
25 laser excites the fluorescent label, emissions are directed to a photomultiplier, and the amount of emitted light is detected and quantitated. The detected signal should be proportional to the amount of probe/target polynucleotide complex at each position of the microarray. The fluorescence microscope can be associated with a computer-driven scanner device to generate a quantitative two-dimensional image of  
30 hybridization intensity. The scanned image is examined to determine the abundance/expression level of each hybridized target polynucleotide.

Typically, microarray fluorescence intensities can be normalized to take into account variations in hybridization intensities when more than one microarray is used under similar test conditions. In a preferred embodiment,



individual probe/target hybridization intensities are normalized using the intensities derived from internal normalization controls contained on each microarray.

Protein or antibody microarray hybridization is carried out essentially as described in Ekins et al. *J Pharm Biomed Anal* 1989, 7: 155; Ekins and Chu, *Clin Chem* 1991, 37: 1955; Ekins and Chu, *Trends in Biotechnology*, 1999, 17, 217-218; 5 MacBeath and Schreiber, *Science* 2000, 289(5485): p. 1760-1763.

### 5. Microarray Expression Profiles

This section describes an expression profile using the polynucleotides of the invention. The expression profile can be used to detect changes in the 10 expression of genes implicated in disease.

The expression profile includes a plurality of detectable complexes. Each complex is formed by hybridization of one or more polynucleotides of the invention to one or more complementary target polynucleotides. At least one of the polynucleotides of the invention, and preferably a plurality thereof, is hybridized to a 15 complementary target polynucleotide forming at least one, and preferably a plurality, of complexes. A complex is detected by incorporating at least one labeling moiety in the complex as described above. The expression profiles provide "snapshots" that can show unique expression patterns that are characteristic of the presence or absence of a disease or condition.

20 After performing hybridization experiments and interpreting detected signals from a microarray, particular probes can be identified and selected based on their expression patterns. Such probe sequences can be used to clone a full-length sequence for the gene or to produce a polypeptide.

The composition comprising a plurality of probes can be used as 25 hybridizable elements in a microarray. Such a microarray can be employed in several applications including diagnostics, prognostics and treatment regimens, drug discovery and development, toxicological and carcinogenicity studies, forensics, pharmacogenomics, and the like.

### 6. Preferred microarrays of the invention

30 The invention provides for microarrays for measuring gene expression characteristic of a cancer of a tissue, comprising at least 4 polypeptide encoding polynucleotides or at least 4 antibodies which bind specifically to the polypeptides encoded by these polynucleotides, as listed in Table 2 and according to the following:

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A microarray for measuring gene expression characteristic of breast cancer comprising markers listed in Table 2 sheet 1; A microarray for measuring gene expression characteristic of uterine cancer comprising markers listed in Table 2 sheet 2; A microarray for measuring gene expression characteristic of kidney cancer comprising markers listed in Table 2 sheet 3; A microarray for measuring gene expression characteristic of bladder cancer comprising markers listed in Table 2 sheet 4; A microarray for measuring gene expression characteristic of lung cancer comprising markers listed in Table 2 sheet 5; A microarray for measuring gene expression characteristic of brain cancer comprising markers listed in Table 2 sheet 6; A microarray for measuring gene expression characteristic of colon cancer comprising markers listed in Table 2 sheet 7; A microarray for measuring gene expression characteristic of intestinal cancer comprising markers listed in Table 2 sheet 8; A microarray for measuring gene expression characteristic of stomach cancer comprising markers listed in Table 2 sheet 9; A microarray for measuring gene expression characteristic of liver cancer comprising markers listed in Table 2 sheet 10; A microarray for measuring gene expression characteristic of pancreatic cancer comprising markers listed in Table 2 sheet 11; and A microarray for measuring gene expression characteristic of spleen cancer comprising markers listed in Table 2 sheet 12.

## B. Immunodiagnosis and polypeptide detection

In certain embodiments, antibodies may be used in characterizing the tissue-specific tumor marker content of healthy and diseased tissues, through techniques such as ELISAs, immunohistochemical detection and Western blotting. This may provide a screen for the presence or absence of malignancy or as a predictor of future cancer. Once the tissue-specific tumor marker is identified, one of skill in the art may produce antibodies against that marker using techniques well known to those of skill in the art

The use of such antibodies in an ELISA assay is contemplated. For example, such antibodies are immobilized onto a selected surface, preferably a surface exhibiting a protein affinity such as the wells of a polystyrene microtiter plate. After washing to remove incompletely adsorbed material, it is desirable to bind or coat the assay plate wells with a non-specific protein that is known to be antigenically

neutral with regard to the test antisera such as bovine serum albumin (BSA), casein or solutions of powdered milk. This allows for blocking of non-specific adsorption sites on the immobilizing surface and thus reduces the background caused by non-specific binding of antigen onto the surface.

5 After binding of antibody to the well, coating with a non-reactive material to reduce background, and washing to remove unbound material, the immobilizing surface is contacted with the biological sample to be tested in a manner conducive to immune complex (antigen/antibody) formation.

Following formation of specific immunocomplexes between the test  
10 sample and the bound antibody, and subsequent washing, the occurrence and even amount of immunocomplex formation may be determined by subjecting same to a second antibody having specificity for the tumor marker that differs from the first antibody. Appropriate conditions preferably include diluting the sample with diluents such as BSA, bovine gamma globulin (BGG) and phosphate buffered saline  
15 (PBS)/Tween. These added agents also tend to assist in the reduction of nonspecific background. The layered antisera is then allowed to incubate for from about 2 to about 4 hr, at temperatures preferably on the order of about 25°C to about 27°C. Following incubation, the antisera-contacted surface is washed so as to remove non-immunocomplexed material. A preferred washing procedure includes washing  
20 with a solution such as PBS/Tween, or borate buffer.

For convenient detection purposes, the second antibody may preferably have an associated enzyme that will generate a color development upon incubating with an appropriate chromogenic substrate. Thus, for example, one will desire to contact and incubate the second antibody-bound surface with a urease or  
25 peroxidase-conjugated anti-human IgG for a period of time and under conditions which favor the development of immunocomplex formation (e.g., incubation for 2 hr at room temperature in a PBS-containing solution such as PBS/Tween).

After incubation with the second enzyme-tagged antibody, and subsequent to washing to remove unbound material, the amount of label is quantified  
30 by incubation with a chromogenic substrate such as urea and bromocresol purple or 2,2'-azino-di-(3-ethyl-benzthiazoline)-6-sulfonic acid (ABTS) and hydrogen peroxide, in the case of peroxidase as the enzyme label. Quantitation is then achieved by measuring the degree of color generation, e.g., using a visible spectrum spectrophotometer.

The preceding format may be altered by first binding the sample to the assay plate. Then, primary antibody is incubated with the assay plate, followed by detecting of bound primary antibody using a labeled second antibody with specificity for the primary antibody.

Immunoblotting and immunohistochemical techniques using antibodies directed against the tumor markers also are contemplated by the invention. The antibodies may be used as high-affinity primary reagents for the identification of proteins immobilized onto a solid support matrix, such as nitrocellulose, nylon or combinations thereof. In conjunction with immunoprecipitation, followed by gel electrophoresis, these may be used as a single step reagent for use in detecting antigens against which secondary reagents used in the detection of the antigen cause an adverse background. Immunologically-based detection methods for use in conjunction with Western blotting include enzymatically-, radiolabel-, or fluorescently-tagged secondary antibodies against the toxin moiety are considered to be of particular use in this regard.

Flow cytometry methods also may be used in conjunction with the invention. Methods of performing flow cytometry are discussed in Zhang *et al.*, *J. Immunology*, 157:3980-3987 (1996) and Pepper *et al.*, *Leuk. Res.*, 22(5):439-444 (1998). Generally, the cells, preferably blood cells, are permeabilized to allow the antibody to enter and exit the cell. If the gene in question encodes a cell surface protein, the step of permeabilization is not needed. After permeabilization, the cells are incubated with an antibody. In preferred embodiments, the antibody is a monoclonal antibody. It is more preferred that the monoclonal antibody be labeled with a fluorescent marker. If the antibody is not labeled with a fluorescent marker, a second antibody that is immunoreactive with the first antibody and contains a fluorescent marker. After sufficient washing to ensure that excess or non-bound antibodies are removed, the cells are ready for flow cytometry. If the marker is an enzyme, the reaction monitoring its specific enzymatic activity either in situ or in body fluids may be performed.

Determining the level of a polypeptide in a sample for the purposes of diagnosis may also be carried out in the form of enzymatic activity testing, when the polypeptide being examined offers such an option.

In addition, whole body image analysis following injection of labeled antibodies against cell surface marker proteins is a diagnostic possibility, as described

above; the detected concentrations of such antibodies are indicative of the sites of tumor/ metastases growth as well as their number and the tumor size.

### C. Carcinogenicity Testing

5           The tissue specific tumor marker genes identified using the methods of the invention can form the basis of a carcinogenicity test. Test agents are evaluated to see if their effects on human cells mimic the effects of loss of the tumor suppressor. Thus the agents are in essence being evaluated for the ability to induce a tumor suppressor mutation, or a mutation in another gene which is in the same regulatory  
10       pathway, or a non-genetic effect which mimics tumor suppressor loss. Test agents which are found to have at least some of the same constellation of effects as tumor suppressor loss on the regulation of the genes identified herein to be tumor suppressor-regulated, are identified as potential carcinogens. Any single gene identified can be used, as can at least 2, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 75, 100,  
15       125, or 150 or more genes identified herein.

          The invention also contemplates the use of the tissue-specific tumor markers identified herein in the screening of compounds for activity in either stimulating tumor suppressor activity, overcoming the lack of a tumor suppressor, or blocking the effect of a mutant tumor suppressor molecule. It is contemplated that any  
20       agent which decreases the expression of a tissue specific tumor marker that was up-regulated upon tumor suppressor inactivation may serve as an anti-tumor agent. Screening assays for such agents are well known to those of skill in the art. U.S. Patent No. 6,262,242 is incorporated herein by reference as providing a general teaching of such screening assays and others relating to the diagnostic and therapeutic  
25       uses of tumor related genes.

## II. Therapeutic Methods of Using Identified Markers

          The genes identified by the invention herein as down-regulated by the loss of a tumor suppressor may prove effective against a given cancer when delivered  
30       therapeutically to the cancer cells. Antisense constructs of the genes identified herein as up-regulated as a result of loss of tumor suppressor can be delivered therapeutically to cancer cells. Other therapeutic possibilities include siRNA or small molecules or antibodies inhibiting the target protein function and/or expression. The goal of such therapy is to retard the growth rate of the cancer cells. Expression of the sense

molecules and their translation products or expression of the antisense mRNA molecules has the effect of inhibiting the growth rate of cancer cells or inducing apoptosis. Sense nucleic acid molecules are preferably delivered in constructs wherein a promoter is operatively linked to the coding sequence at the 5'-end and initiates transcription of the coding sequence. Anti-sense constructs contain a promoter operatively linked to the coding sequence at the 3'-end such that upon initiation of transcription at the promoter an RNA molecule is transcribed which is the complementary strand from the native mRNA molecule of the gene.

Delivery of nucleic acid molecules can be accomplished by many means known in the art. Gene delivery vehicles are available for delivery of polynucleotides to cells, tissue, or to a mammal for expression. For example, a polynucleotide sequence of the invention can be administered either locally or systemically in an expression construct or vector. There are a number of ways in which expression vectors may be introduced into cells. In certain embodiments of the invention, the expression construct comprises a virus or engineered construct derived from a viral genome. In other embodiments, non-viral delivery is contemplated. The ability of certain viruses to enter cells via receptor-mediated endocytosis, to integrate into host cell genomes and express viral genes stably and efficiently have made them attractive candidates for the transfer of foreign genes into mammalian cells (Ridgeway, In: *Vectors: A survey of molecular cloning vectors and their uses*, Rodriguez R L, Denhardt D T, eds. Stoneham: Butterworth, pp. 467-492, 1988; Nicolas *et al.*, In: *Vectors: A survey of molecular cloning vectors and their uses*, Rodriguez & Denhardt (eds.), Stoneham: Butterworth, pp. 493-513, 1988; Baichwal *et al.*, In: *Gene Transfer*, Kucherlapati ed., New York, Plenum Press, pp. 117-148, 1986; Temin, In: *gene Transfer*, Kucherlapati (ed.), New York: Plenum Press, pp. 149-188, 1986). The viral vector can also be an astrovirus, coronavirus, orthomyxovirus, parvovirus, paramyxovirus, parvovirus, picornavirus, poxvirus, togavirus viral vector. See generally, Jolly, *Cancer Gene Therapy* 1:51-64 (1994); Kimura, *Human Gene Therapy* 5:845-852 (1994), Connelly, *Human Gene Therapy* 6:185-193 (1995), and Kaplitt, *Nature Genetics* 6:148-153 (1994).

Several non-viral methods for the transfer of expression constructs into cultured bacterial cells are contemplated by the invention. This section provides a discussion of methods and compositions of non-viral gene transfer. DNA constructs of the invention are generally delivered to a cell and, in certain situations, the nucleic

acid or the protein to be transferred may be transferred using non-viral methods. The non-viral methods include calcium phosphate precipitation (Graham *et al.*, *Virology*, 52:456-467, 1973; Chen *et al.*, *Mol. Cell. Biol.*, 7:2745-2752, 1987; Rippe *et al.*, *Mol. Cell Biol.*, 10:689-695, 1990) DEAE-dextran (Gopal, *Mol. Cell Biol.*, 5:1188-1190, 1985), electroporation (Tur-Kaspa *et al.*, *Mol. Cell Biol.*, 6:716-718, 1986; Potter *et al.*, *Proc. Nat. Acad. Sci. USA*, 81:7161-7165, 1984), direct microinjection (Harland and Weintraub, *J. Cell Biol.*, 101:1094-1099, 1985.), DNA-loaded liposomes (Nicolau and Sene, *Biochim. Biophys. Acta*, 721:185-190, 1982; Fraley *et al.*, *Proc. Natl. Acad. Sci. (USA)*, 76:3348-3352, 1979; Felgner, *Sci Am.* 276(6):102-6, 1997; Felgner, *Hum Gene Ther.* 7(15):1791-3, 1996), cell sonication (Fechheimer *et al.*, *Proc. Natl. Acad. Sci. (USA)*, 84:8463-8467, 1987), gene bombardment using high velocity microprojectiles (Yang *et al.*, *Proc. Natl. Acad. Sci USA*, 87:9568-9572, 1990), conjugation (Gavigan *et al.* In: *Mycobacteria Protocols*, Tanya Parish and Neil G. Stoker (eds). pp. 119-128 1998. Humana Press, Twtowa, NJ) and receptor-mediated transfection (Wu *et al.*, *J. Biol. Chem.*, 262:4429-4432, 1987; Wu *et al.*, *Biochemistry*, 27:887-892, 1988; Wu *et al.*, *Adv. Drug Delivery Rev.*, 12:159-167, 1993).

The expression construct also may be entrapped in a liposome. Liposomes that can act as gene delivery vehicles are described in U.S. Pat. No. 5,422,120, PCT Patent Publication Nos. WO 95/13796, WO 94/23697, and WO 91/144445, and EP No. 524,968. The addition of DNA to cationic liposomes causes a topological transition from liposomes to optically birefringent liquid-crystalline condensed globules (Radler *et al.*, *Science*, 275(5301):810-4, 1997). These DNA-lipid complexes are potential non-viral vehicles for use in gene delivery.

Also contemplated in the invention are various commercial approaches involving "lipofection" technology. In certain embodiments of the invention, the liposome may be complexed with a hemagglutinating virus (HVJ). This has been shown to facilitate fusion with the cell membrane and to promote cell entry of liposome-encapsulated DNA (Kaneda *et al.*, *Science*, 243:375-378, 1989). In other embodiments, the liposome may be complexed or employed in conjunction with nuclear nonhistone chromosomal proteins (HMG-1) (Kato *et al.*, *J. Biol. Chem.*, 266:3361-3364, 1991).

Receptor-mediated gene targeting vehicles generally consist of two components: a cell receptor-specific ligand and a DNA-binding agent. Several ligands have been used for receptor-mediated gene transfer. The most extensively

characterized ligands are asialoorosomucoid (ASOR) (Wu *et al.*, 1987, *supra*) and transferrin (Wagner *et al.*, *Proc. Natl. Acad. Sci. USA*, 87(9):3410-3414, 1990). Recently, a synthetic neoglycoprotein, which recognizes the same receptor as ASOR, has been used as a gene delivery vehicle (Ferkol *et al.*, *FASEB J.*, 7:1081-1091, 1993; 5 Perales *et al.*, *Proc. Natl. Acad. Sci. USA*, 91:4086-4090, 1994) and epidermal growth factor (EGF) has also been used to deliver genes to squamous carcinoma cells (Myers, EPO 0273085).

Another embodiment of the invention for transferring a naked DNA expression construct into cells may involve particle bombardment. This method 10 depends on the ability to accelerate DNA coated microprojectiles to a high velocity, allowing them to pierce cell membranes and enter cells without killing them (Klein *et al.*, *Nature*, 327:70-73, 1987). Exemplary naked DNA introduction methods are described in PCT Patent Publication No. WO 90/11092 and U.S. Pat. No. 5,580,859. Several devices for accelerating small particles have been developed. One such 15 device relies on a high-voltage discharge to generate an electrical current, which in turn provides the motive force (Yang *et al.*, *Proc. Natl. Acad. Sci. USA*, 87:9568-9572, 1990). The microprojectiles used to date have consisted of biologically inert substances such as tungsten or gold beads.

20

### Example 1

#### Validation of the methods of the invention in LNCAP cells

The present Example demonstrates the methods of identifying tissue- 25 specific tumor markers that are negatively regulated by a tumor suppressor. In the present Example, it was demonstrated for the first time that the expression of PSA is negatively regulated by p53.

Prostate cancer, the most frequently diagnosed malignancy in men in western countries (*Cancer*, 71(Suppl.): 880-886, 1993), is often characterized by 30 elevated prostate-specific antigen (PSA) secretion that is broadly used as a blood-borne diagnostic marker of the disease. PSA is synthesized exclusively in prostate epithelia by normal, hyperplastic and malignant cells, and its levels are seen to rise several-fold above background in the blood as a result of benign prostatic



hyperplasia. The levels of PSA in the serum of individuals at end-stage metastatic prostate carcinoma may be more than a hundred times higher than normal levels of the marker (Kim and Logothetis, *Urol. Clin. North Am.*, 26:281-290 1999; Abate-Shen and Shen, *Genes Dev.*, 14:2410-2434, 2000). Expression of the PSA gene was demonstrated to be directly regulated by binding of androgen receptor (AR) (Young *et al.*, *Cancer Res.*, 51:3748-3752 1991; Montgomery *et al.*, *Prostate*, 21:63-73, 1992; Trapman and Cleutjens, *Semin. Cancer Biol.*, 8:29-36 1997) to three androgen responsive elements (AREs) identified within the 5.8 kb PSA promoter (Schnur *et al.*, *Urology*, 162:2040-2045 1996; Cleutjens *et al.*, *Mol. Endocrinol.*, 11:148-161, 1997; Zhang *et al.*, *Biochem. Biophys. Res. Comm.*, 231:784-788, 1997; Zhang *et al.*, *Nucleic Acids Res.*, 25:3143-3150, 1997). However, detailed analyses of PSA promoter activity in androgen-dependent and androgen-independent prostate carcinoma cell lines indicated that the control of transcription of the PSA gene is not limited to androgen regulation (Yeung *et al.*, *J. Biol. Chem.*, 275:40846-40855 2000).

The present Example provides evidence showing the involvement of p53 tumor suppressor in regulation of PSA promoter. Micro-array hybridization and analyses were performed using LNCaP cells. This cell line originally isolated from lymph node metastases of prostate adenocarcinoma, retains wild type p53, androgen dependence and expression of a variety of prostate-specific markers, all known as properties of a relatively early stage of prostate cancer progression. Inactivation of p53 function by a dominant negative mutant in these cells imitates an important step in tumor progression and allows analysis of the genetic basis for altered tumor cell phenotype associated with p53 suppression.

A variant of LNCaP cells with inactivated p53, LN-56 (Rokhlin *et al.*, *Oncogene*, 19:1959-1968, 2000), was generated by transduction of retroviral construct expressing the potent dominant negative p53 mutant, GSE56 (Ossovskaya *et al.*, *Proc. Natl. Acad. Sci. USA*, 93:10309-10314, 1996). GSE56-mediated inactivation of p53 resulted in resistance to apoptosis and increased tumorigenicity of LN-56 cells (Rokhlin *et al.*, *Oncogene*, 19:1959-1968, 2000), suggesting that p53 is at least partially functional in LNCaP cells. Moreover, both steady-state and inducible expression level of p53-responsive gene p21/waf1 were reduced in LN-56 cells.

PSA was among the genes that showed the most pronounced differential expression in LNCaP versus LN-56 cells. PSA was expressed four times higher in LN-56 than in LNCaP cells. To determine whether differences in mRNA

expression correlated with PSA protein expression, the amount of secreted PSA in the medium from LNCaP and LN-56 cells was determined. This revealed that the latter cells produced 6-8 times more PSA as compared to LNCaP (Figure 1). These observations suggested that expression of PSA gene is likely to be under the negative regulatory control of p53 and that elevated expression of PSA in advanced prostate cancer may be indicative for p53 suppression.

To determine whether p53 directly affects transcription from the PSA promoter, a CAT assay was performed in the LNCaP cells transfected with the reporter constructs containing the CAT gene under the control of the proximal PSA promoter (nucleotides -407 to +11) linked to the PSA enhancer element (nucleotides -5322 to -3740). This construct was previously shown to imitate the endogenous PSA gene regulation (Zhang *et al.*, *Biochem. Biophys. Res. Comm.*, 231:784-788, 1997; Zhang *et al.*, *Nucleic Acids Res.*, 25:3143-3150, 1997). Since PSA transcription is also known to be androgen dependent, for these studies, LNCaP cells that retain androgen dependence were used. To increase the wild type p53 activity, different amounts of wild type p53 expression plasmid were cotransfected with the PSA-reporter vector. To inhibit endogenous p53 function, cotransfection with the GSE56-expressing plasmid was employed (Ossovskaya *et al.*, *Proc. Natl. Acad. Sci. USA*, 93:10309-10314, 1996). Another reporter construct containing the CAT reporter gene under the control of p53-responsive promoter carrying the p53-binding site from p21/Waf1 gene was used to monitor the p53 activity in transfected cells.

Introduction of different amounts of wild type p53-expressing plasmid into LNCaP cells resulted in dose-dependent changes of CAT activity driven from both p21- and PSA-derived promoter elements, though in opposite directions: while the p21 promoter construct was activated, expression of the PSA reporter was suppressed by p53. When GSE56 was co-transfected with either of the reporter constructs, an inverted picture was observed (Figure 2).

Sequence analysis does not reveal any canonical p53 binding sites within or in the vicinity of the PSA promoter region and in the first intron of the PSA gene. It is noteworthy that most of the known p53-repressed genes also do not possess such sites in their promoter regions and do not necessarily require p53.

Since it has previously been shown that negative regulation of transcription by p53 may involve p53-mediated recruitment of histone deacetylases (HDAC) (Murphy *et al.*, *Genes Dev.*, 13:2490 -2501 1999), the inventors set out to

determine whether this would be also true for the PSA promoter. Following co-transfection of PSA-CAT reporter and wild type p53-expressing plasmids, the LNCaP cells were treated with the HDAC inhibitor trichostatin A (TSA) for 24 h and the lysates of transfected cells were tested for CAT activity. These experiments demonstrated that TSA completely abrogated the p53-mediated repression of PSA promoter driven transcriptional activity. At the same time, TSA had no effect on p53-mediated transactivation as determined in a similar experiment employing the p21 promoter-driven CAT reporter construct (Figure 3). Thus, the PSA gene can be added to a growing list of genes that are negatively regulated by p53 through HDAC-mediated transcriptional repression.

Use of a potent dominant negative p53 inhibitor, GSE56, allowed the determination of the p53 dependence of PSA expression. However, this mutant form does not naturally occur in human tumors. In order to more adequately imitate events naturally occurring in the course of tumor progression, the effect of four tumor-derived p53 mutants (135Val, 141Ala, 156Pro and 175His), two of which are frequent types of p53 mutants in prostate cancer (141Ala and 175His), on expression of PSA was determined. LNCaP cells were transduced with retroviruses expressing the above p53 mutant variants and the level of PSA was measured in the medium conditioned by each type of the transduced cell populations. In parallel, the potential suppressive effect of the introduced p53 mutants on the activity of endogenous p53 in LNCaP cells was estimated by monitoring the p53-dependent p21 induction in response to doxorubicin treatment (Rokhlin *et al.*, *Oncogene*, 19:1959-1968, 2000). As seen in Figure 4, only one of the tested mutants, 175His, displayed a strong dominant negative activity against the wild type p53 reflected by the lack of p21 induction by DNA damage. Val135 mutant showed marginal p53 suppression, while the two remaining mutants did not interfere with p53-mediated p21 induction at all. Remarkably, this pattern of anti-p53 activity was exactly mirrored in the pattern of PSA expression: compared to control, 175His expressing cells produced 9-11 times more PSA, whereas in 135Val cells its level was slightly increased and 141Ala, 156Pro.

The list of genes whose expression was changed following wild type p53 suppression in LNCaP cells is attached as Table 1.

In conclusion, this Example demonstrate that the transcription of PSA gene in the prostate carcinoma cell line, LNCaP, is under strict negative control of

p53 and its expression can be greatly activated by suppression of wild type p53 activity. Since LNCaP is considered most adequate and conventional among available *in vivo* models of hormone-dependent prostate cancer, these results likely reflect regulation of PSA in naturally occurring tumors. Thus, one of the most useful diagnostic tumor markers is, in fact, a tissue specific indicator of p53 inactivation in prostate cells. Being dependent on p53 inactivation, elevated production of PSA may therefore be indicative for the ongoing selection of p53-deficient cell variants with the broken control of apoptosis, angiogenesis, and genomic stability, all normally regulated by wild type p53. In fact, the loss of functional p53 by LNCaP cells is accompanied not only by elevated PSA secretion but also by acquisition of high tumorigenicity and resistance to TNF (Rokhlin *et al.*, *Oncogene*, 19:1959-1968, 2000).

For further detail concerning the above Example, see the inventors' publication: Gurova et al: Expression of prostate specific antigen (PSA) is negatively regulated by p53. *Oncogene* 2002, 21: 153-157.

## Example 2

### Validation of the methods of the invention in sets of p53<sup>-/-</sup> and p53 wild-type tissues and identification of new cancer markers

The most desirable characteristics of an ideal tumor marker involve tissue/organ specificity of expression and association with definite type of tumor and/or stage of tumor progression. Alternatively, tumor markers may be ubiquitously highly expressed in numerous tumors displaying low expression or lack of expression in normal tissues. Prospective markers can be oncogenes themselves, and thus be directly involved in malignant transformation (i.e., BCR-ABL in Ph<sup>+</sup>-positive CML and ALL) (Daley et al., *Science* 1990 Feb 16;247(4944):824-30.) On the other hand, the marker genes may be not the active players in carcinogenesis, their overexpression being a consequence of transformation-associated changes in gene regulation. Genes from the first group may be targets for functional inhibition via direct targeting by drugs, whereas the genes (proteins) from the second group, if localized to the plasma membrane, may be used for targeting of tumor cells via specific antibodies-mediated strategies. Changes in the expression of these genes may also be used as a readout for the establishment of bioassay for the purpose of screening for anti-cancer drugs, e.g. targeted at reactivation of normal tumor suppressor gene function. Marker proteins

from both groups may serve also as early diagnostic or progressive tumor markers if found in body fluids (i.e., like PSA in the cancer of prostate). Alternatively they may serve as differential diagnosis markers during morphological examination of tumor samples or tissue biopsies.

5 The invention provides a systematic approach for the search of cancer marker genes. This approach is based on the idea that many such genes may be transcriptionally activated in tissues following the loss of the most common tumor suppressor genes like e.g., p53, PTEN, RB, and p16/p19 and that this regulation will be conserved in normal and tumor cells from the same origin. Technically, the gene  
10 discovery may be performed by comparison of gene expression profiles in the fitted tissue pairs derived from normal and genetically modified mice, like i.e. p53 <sup>-/-</sup> mice, p16/p19<sup>-/-</sup> mice, tissues with targeted expression of SV40 large T antigen that simultaneously inactivates both RB and p53 function (TRAMP mice, expressing LT-Ag in prostate). There are some literature indications, as well as examples that support  
15 the feasibility of such an approach. For example, it was demonstrated wild-type p53 can suppress the expression of two neoangiogenesis and progression-related genes known to be highly expressed in tumors, COX2 (Subbaramaiah et al., J Biol Chem 1999 Apr 16;274(16):10911-5) and VEGF (Zhang et al., *Cancer Res* 2000 Jul 1;60(13):3655-61.) Both genes are currently regarded as targets for anti-cancer  
20 therapeutics. However, the connection of COX2 and VEGF to p53 was found long after they were first discovered and their function and tumor association were well established.

In the present studies presented in Example 1 above, the inventors created an isogenic pair of LNCaP prostate tumor cell lines differing in their p53  
25 status and applied cDNA microarray analysis to look for differentially expressed genes. It was discovered that the baseline expression of several known tumor markers is significantly elevated in LNCaP cells that lack functional p53 protein compared to the same cells that express wt p53. These genes include e.g., COX2, tumor-specific heparin-binding growth factor midkine (possesses angiogenic and anti-apoptotic properties) (Ikematsu et al., *Br J Cancer* 2000 Sep;83(6):701-6), tumor tissue  
30 associated hyaluronan receptor CD44 (Sneath et al., *Mol Pathol*. 1998 Aug;51(4):191-200) and PSA (prostate specific antigen).

COX2 inhibitors are currently in clinical trials against prostate cancer. Midkine was immunohistochemically shown to be expressed specimens 86.3% of

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prostate cancer specimen examined, with metastatic lesions generally showing higher expression than the corresponding primaries; normal prostate tissues were negative or showed only weak staining. Midkine was also detected in 12 of 15 latent cancers (80%) and in 12 of 16 cases of PIN (75%) (Konishi et al., *Oncology* 1999 Oct;57(3):253-7). PSA is the major currently used prostate cancer diagnostic marker. In Example 1 it is shown that its promoter is directly suppressed by wt p53, thus PSA up-regulation in prostate cancer may be indicative for the wt p53 loss. The list of genes which expression was changed following wt p53 suppression in LNCaP cells is attached in the accompanying Excel file (Table 1). The inventors concluded that general proof of concept is achieved and embarked upon a large-scale experiment involving microarray-based comparison of gene-expression profiles in the tissue pairs derived from normal and p53<sup>-/-</sup> mice.

Poly A RNA was extracted from spleen, pancreas, liver, stomach, intestine, colon, lung, brain, bladder, kidney, placenta/uterus and mammary glands of normal and p53-deficient mice and used for fluorescently-labeled probes for microarray hybridizations. All tissue-specific probes were labeled with Cy5 fluorescent marker, while the common control probe (an equal proportion mixture of all the RNAs) was labeled with Cy3. The common control probe was used in order to assess also the tissue-specificity of gene expression. All probes were hybridized to MouseGEM (Incyte). Upon quality control and pair-wise balancing of Cy5 and Cy3 signals, the differential (against common control) gene expression levels were normalized between p53<sup>-/-</sup> tissues and their corresponding normal counterparts. As a result the inventors obtained a table of genes containing their differential expression levels in p53<sup>-/-</sup> tissues compared to the corresponding normal tissues; the genes were sorted according to their expression levels in one particular tissue from maximally up-regulated genes to maximally down-regulated ones (Table 2). Genes showing absolute differential expression levels less than 1.9 were excluded from these tables. Thus, these tables contain the lists of genes with maximal differential tissue-specific expression in p53-deficient mice. It must be noted, that the majority of identified genes has changed their expression in a tissue-specific manner, though some of them like, e.g., choline kinase (known to be up-regulated and activated in numerous cancer types) was up-regulated in p53<sup>-/-</sup> pancreas, stomach, intestine, lung, bladder, uterus, and mammary gland. Another interesting observation is that there was almost no

overlap between the list of genes that were up- or down-regulated in different p53<sup>-/-</sup> tissues.

- Out of the approximately 10,000 genes printed on the microarray, approximately 445 genes that were found to be up-regulated in p53<sup>-/-</sup> tissues were studied in further detail, as they had the largest potential of serving as tumor markers (drug targets and diagnostic markers). These genes appear in the Excel file, Table 3. This table combines the p53-dependent differential expression data with the tissue specificity of gene expression data. The actual differential expression of genes in regard to common control is also presented. As discussed above, the markers are based on genes that are: either
1. up-regulated in a certain p53<sup>-/-</sup> tissue and are normally expressed predominantly in this tissue; or
  2. normally expressed at low levels in one or several tissues but are up-regulated in one or numerous p53<sup>-/-</sup> tissues.

- As evident from Table 3, genes belonging to both groups were identified. For example, Mest-linked imprinted transcript, anonymous brain protein, and potassium voltage-gated channel (subfamily Q, member2) are specifically expressed in brain and are up-regulated in p53<sup>-/-</sup> brain compared to the normal one. Another example: expression of liver-specific fatty acid transporter, betaine-homocystein methyltransferase and of several unknown genes (ESTs) is significantly increased in p53<sup>-/-</sup> hepatic tissue. On the other hand, genes such as choline kinase that is usually expressed at low levels is significantly enhanced in numerous p53<sup>-/-</sup> tissues (see above). A similar behavior is also observed i.e. for EGF (enhanced in p53<sup>-/-</sup> bladder and mammary gland); carbonic anhydrase 6 (enhanced in p53<sup>-/-</sup> bladder); zinc finger protein 101 (enhanced in p53<sup>-/-</sup> liver). Numerous unknown genes (ESTs) also fall in this the most promising category.

- The approximately 445 genes identified as up-regulated in p53<sup>-/-</sup> mice were further prioritized for the purpose of serving as diagnostic markers; the highly preferred diagnostic markers are presented in Table 5 (general cancer markers) and Table 6 (tissue-specific cancer markers). Thus, of the approximately 10,000 genes printed on the array, the inventors were able to select through the methods of the invention a total of 338 genes ideally suited for several diagnostic and prognostic uses in various cancers, as described herein.

Table 4 sheet 1 provides a list of 32 genes/ polypeptides identified according to the methods of the present example as disclosed herein that are known in the art to be markers for certain cancers, thus validating the effectiveness of the methods of the invention. This table also includes the PubMed indexing numbers of  
5 publications that disclose the connection of these genes/ polypeptides to cancer.

In summary, the inventors provide a list of genes characterized in regard to tissue-specificity of their normal expression and induction/reduction in various p53-deficient tissues. A similar expression pattern should be preserved in tumor cells originating from the same tissue. Thus, the identified genes may serve as  
10 tumor markers.

### Example 3

#### Validation data for additional tumor suppressor genes

The methods of the invention, as validated in example 2, are not  
15 limited only to the use of the tumor suppressor p53, as any other tumor suppressor gene with confirmed involvement in a specific type of cancer may be involved in negative regulation of tissue specific genes by direct (i.e., transcription factors) or indirect (i.e., signaling pathway members) pathways.

The inventors therefore proceeded to test these methods on p53  
20 knockout mice, TRAMP mice and PTEN hemisigous mice (the complete knockout is non-viable). TRAMP transgenic mice express large T-antigen of SV40 under the control of prostate-specific probasin promoter (Jackson labs), and have both tumor suppressor genes p53 and Rb inactivated. PTEN hemisigous mice have only one allele of the tumor suppressor gene PTEN. The experiments were carried out on prostate  
25 cells. For each hybridization, RNA was isolated from prostates of 6-8 males of different age in dependence of genotype prior to appearance of initial signs of hyperplasia of prostate according to published data (p53KO, TRAMP and corresponding control C57BL6 mice - 9-10 weeks old, PTEN and corresponding control FVB mice - 6 weeks old). Total RNA was isolated from each prostate  
30 separately from 6-8 animals of each genotype. In total two probes for each genotype were prepared and hybridized with a set of three mouse Affymetrix arrays which cover the majority of known mouse transcripts. Genes with reproducible 2 fold overexpression in tumor suppressor gene deficient prostates as compared with wild



type organs (confirmed specific hybridization) in both two repetitive hybridizations were picked for identification of human homologs.

Remarkably, among 161 genes picked for further analysis, more than 10 were found to be either known or candidate cancer markers although their p53 or Rb dependence had not been previously determined (see Table 4 sheet 2). A significant proportion of other genes that came out of these experiments are known as genes with melanoma or glioma-specific expression that is consistent with frequent acquisition of traces of neuroendocrinal differentiation by prostate cancer cells. Additional genes/ polypeptides previously linked to cancer and identified according to the method described in this Example include: KIAA430, limkainb1 (NP\_596912), that associates with the LIM-kinase 2, which may be critical for metastasis (PMID: 11208874); Glutamate-cystein ligase (modifier subunit), the rate-limiting enzyme in glutathione synthesis, that is overexpressed in numerous tumor types (PMID: 11774239, 11753966); PCNA (proliferating cells nuclear antigen), an auxiliary protein of DNA polymerase delta that is involved in the control of eukaryotic DNA replication, and overexpressed in numerous cancer types (e.g., PMID: 12145573, 12046056, PMID: 11750711, 11606074); Mcm5, a DNA replication licensing factor under transcriptional control of E2F (PMID: 10327050), (abolishment of Rb function by TRAMP), which is a known marker for cancer (PMID: 2122098, 11839717, 10551502, 9843993); Transducin-like enhancer protein 2 (TLE2), a Nuclear effector molecule and neural/neuroectodermal associated gene overexpressed in synovial sarcoma (PMID: 12414507); Inhibitor of DNA binding 1 (ID1), a negative regulator of helix-loop-helix DNA binding proteins with the following functions: required to maintain the timing of neuronal differentiation in the embryo and invasiveness of the vasculature (hence, neurogenesis and vasculogenesis) (PMID: 10537105), inhibits transcription of trombospondin-1, thus promoting angiogenesis (PMID: 12498716), helps to keep neuroblastoma cells in an undifferentiated state (PMID: 11756408), directly inhibits expression of p16 via repression of Ets and E-protein-mediated transactivation (PMID: 11427735), trichostatin A treatment of ovarian cancer cells causes decrease of Rb phosphorylation and reduction of ID1 expression (thus the observed expression pattern in TRAMP mice is concomitant with Rb inactivation by T-Ag) (PMID: 12479699). This gene has several known associations to cancer: associated with grade and invasiveness of endometrial carcinoma (PMID: 11275368), upregulated in early melanomas (if not, p16 is mutated) (PMID: 11507043),

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expressed in astrocytes and endothelial cells within astrocytomas positively correlating with stage and grade (PMID: 12007145).

These preliminary results clearly support the main concept of the instant invention, and demonstrate that cancer markers can be frequently found among  
5 the genes that are normally under the negative control of tumor suppressors.

Table 4 sheet 2 provides a list of 12 genes/ polypeptides identified according to the methods of the present Example and of Example 2 as disclosed herein that are known in the art to be markers for certain cancers, thus validating the effectiveness of the methods of the invention. This table also includes the PubMed  
10 indexing numbers of publications that disclose the connection of these genes to cancer.

While the invention has been described in terms of specific embodiments, it is understood that variations and modifications will occur to those  
15 skilled in the art. Accordingly, only those limitations appearing in the appended claims should be placed upon the invention. The entire disclosure of all publications and patents cited herein are hereby incorporated by reference.

RowType	GeneDescription	GeneID	LN56 DIFF
gene	Human clone 23586 mRNA sequence. (Incyte PD:530629)	530629	6.6
gene	ESTs, Moderately similar to III, ALU SUBFAMILY J, WARNING ENTRY_III_LH, sapiens. (Incyte PD:855928)	855928	5.5
gene	Fc fragment of IgG, low affinity IIa, receptor for (CD16). (Incyte PD:1560730)	1560730	5
gene	prostaglandin-endoperoxide synthase 2, (prostaglandin_GH synthase_and_cyclooxygenase), (incyte PD:3139163)	3139163	4.9
gene	Human GABA-A receptor, pi subunit, mRNA, complete cds. (Incyte PD:1824443)	1824443	4.8
gene	kallikrein 3, (prostate specific antigen). (Incyte PD:1655492)	1655492	4.6
gene	regulator of G-protein signaling 2, 24KD. (Incyte PD:1218114)	1218114	4.5
gene	Human tumor, necrosis factor-inducible (TSG-6), mRNA, fragment, adhesion receptor, CD44, putative. CDS. (Incyte PD:3142364)	3142364	4
gene	ESTs, Moderately similar to III, ALU SUBFAMILY SC, WARNING ENTRY_III_LH, sapiens. (Incyte PD:2458029)	2458029	3.6
gene	ESTs (Incyte PD:1305355)	1305355	3.6
gene	ESTs (Incyte PD:2740865)	2740865	3.5
gene	butyrylcholinesterase. (Incyte PD:1599272)	1599272	3.5
gene	ESTs, Weakly similar to X-linked retinopathy protein. (Incyte PD:2311432)	2311432	3.3
gene	ESTs (Incyte PD:2423162)	2423162	3.3
gene	ESTs (Incyte PD:1965673)	1965673	3.3
gene	ESTs (Incyte PD:3519565)	3519565	3.2
gene	ESTs (Incyte PD:1537925)	1537925	3.2
gene	bactericidal/permeability-increasing protein. (Incyte PD:406016)	406016	3.2
gene	ellogiprenin_1. (Incyte PD:4216520)	4216520	3.1
gene	ESTs (Incyte PD:944140)	944140	3.1
gene	KIAA0025 gene product. (Incyte PD:2054420)	2054420	3.1

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ESTs_Moderately similar to IIII_ALU_SUBFAMILY_SP_WARNING_ENTRY_III [H.sapiens] (Incyle PD:1574536)	3.1	1574536
ESTs (Incyle PD:966948)	3	966948
ESTs_Weakly similar to (define_not_available_4580662) [H.sapiens] (Incyle_PD:3749894)	3	3749894
ESTs (Incyle PD:2045819)	3	2045819
ESTs (Incyle PD:979945)	3	979945
ESTs (Incyle PD:2149058)	3	2149058
prostaglandin E receptor 4 (subtype EP4) (Incyle PD:1631793)	3	1631793
ESTs (Incyle PD:3252857)	3	3252857
ESTs_Moderately similar to IIII_ALU_SUBFAMILY_SX_WARNING_ENTRY_III [H.sapiens] (Incyle PD:2447969)	2.9	2447969
ESTs (Incyle PD:1397926)	2.9	1397926
fizzled (Drosophila) homolog 5 (Incyle PD:3129290)	2.9	3129290
ATPase_Na/K+ transporting, alpha 2 (+ polypeptide (Incyle PD:1622542)	2.8	1622542
Human desmocollin-2 mRNA, 3' UTR (Incyle PD:1403294)	2.8	1403294
N-acetylglucosaminidase_alpha- (Incyle PD:1664863)	2.8	1664863
protease inhibitor 12 (neuroserpin) (Incyle PD:2716511)	2.8	2716511
ESTs (Incyle PD:2556708)	2.7	2556708
KIAA0075 gene product (Incyle PD:3094261)	2.7	3094261
ESTs (Incyle PD:1824332)	2.7	1824332
Homo sapiens mRNA, chromosome_1 specific, transcript KIAA0495 (Incyle PD:1963554)	2.7	1963554
ESTs (Incyle PD:2287483)	2.7	2287483
ESTs (Incyle PD:3144018)	2.7	3144018
ESTs (Incyle PD:2466668)	2.6	2466668
ESTs (Incyle PD:2396970)	2.6	2396970
ESTs (Incyle PD:2748370)	2.6	2748370
ESTs_Weakly similar to IIII_ALU_SUBFAMILY_SC_WARNING_ENTRY_III [H.sapiens] (Incyle PD:2243954)	2.6	2243954
transcription_factor_3_1 (E2A, Immunoglobulin enhancer binding factors, E12/E47) (Incyle PD:1640174)	2.6	1640174
Not mapped (Incyle PD:3463468)	2.6	3463469
ESTs (Incyle PD:201053)	2.6	201053
ESTs (Incyle PD:865723)	2.6	865723
adrenergic_beta2-, receptor, surface (Incyle PD:3200341)	2.6	3200341

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gene	solute_carrier_family_12_(sodium/chloride_transporters)_member_3_(incyte_PD-3535415)	3535415	2.5	
gene	ESTs (incyte_PD-4061967)	4061967	2.4	
gene	ESTs_Highly_similar_to_III_ALU_SUBFAMILY_SP_WARNING_ENTRY_III_H.sap			
gene	ESTs (incyte_PD-966692)	966692	2.4	
gene	Not mapped (incyte_PD-2542313)	2542313	2.4	
gene	ESTs (incyte_PD-1911371)	1911371	2.4	
gene	ESTs_Moderately_similar_to_III_ALU_SUBFAMILY_J_WARNING_ENTRY_III_H.sapiens (incyte_PD-2049587)	2049587	2.4	
gene	ESTs_Moderately_similar_to_protein_serine/threonine_kinase_H.sapiens (incyte_PD-2789518)	2789518	2.4	
gene	ataxia_telangiectasia_mutated_includes_complementation_groups_A_C_and_D_1 (incyte_PD-394665)	394665	2.4	
gene	Not mapped (incyte_PD-2477854)	2477854	2.4	
gene	Not mapped (incyte_PD-2312442)	2312442	2.4	
gene	10D repeat domain 2 (incyte_PD-2210264)	2210264	2.4	
gene	Human_cytochrome_P450-11B (H1B3)_mRNA_complete_cds (incyte_PD-2796468)	2796468	2.4	important for growth of some
gene	dopa_decarboxylase (aromatic L-amino acid decarboxylase) (incyte_PD-2820985)	2820985	2.4	cardio tumors
gene	potassium_channel_subfamily_K_member_1 (TWIK-1) (incyte_PD-1479255)	1479255	2.4	
gene	ESTs (incyte_PD-2289801)	2289801	2.3	
gene	ESTs (incyte_PD-1602726)	1602726	2.3	
gene	primase_polypeptide_1 (48kD) (incyte_PD-105121)	105121	2.3	
gene	ESTs (incyte_PD-2230152)	2230152	2.3	
gene	midkine (neurite growth-promoting factor 2) (incyte_PD-940845)	940845		cyclone expressed by numerous
gene	ESTs (incyte_PD-2149237)	2149237		types of tumors. Our candidate in
gene	ESTs (incyte_PD-1817969)	1817969	2.3	TCC
gene	ESTs (incyte_PD-1753445)	1753445	2.3	
gene	ESTs (incyte_PD-2882960)	2882960	2.2	
gene	ESTs (incyte_PD-213516)	213516	2.2	
gene	ESTs (incyte_PD-2359527)	2359527	2.2	
gene	ESTs_Highly_similar_to_gelatinase_4589636_H.sapiens (incyte_PD-2499488)	2499488	2.2	

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gene	ESTs (incyte PD:2662127)	2662127	2,2
gene	ESTs (incyte PD:2544622)	2544622	2,2
gene	Human clone 23908 mRNA sequence (incyte PD:2251851)	2251851	2,2
gene	phorbol (similar to apolipoprotein B mRNA editing protein) (incyte PD:212573)	212573	2,2
gene	platelet-activating factor receptor (incyte PD:2966535)	2966535	2,2
gene	EST (incyte PD:2448338)	2448338	2,2
gene	ESTs (incyte PD:2136337)	2136337	2,2
gene	ESTs (incyte PD:4003220)	4003220	2,2
gene	ESTs (incyte PD:2667106)	2667106	2,2
gene	ESTs, Weakly similar to III <sub>1</sub> ALU SUBFAMILY_J WARNING_ENTRY_III <sub>1</sub> [H.sapi]	465501	2,2
gene	ensl (incyte PD:465591)	465591	2,2
gene	ESTs (incyte PD:2372541)	2372541	2,2
gene	E2F transcription factor 6 (incyte PD:14588)	14588	2,2
gene	ESTs (incyte PD:2598965)	2598965	2,2
gene	ESTs, Weakly similar to III <sub>1</sub> ALU SUBFAMILY_SB WARNING_ENTRY_III <sub>1</sub> [H.sapi]	2075469	2,2
gene	ensl (incyte PD:2075469)	2075469	2,2
gene	ESTs (incyte PD:2296027)	2296027	2,2
gene	Not mapped (incyte PD:2896792)	2896792	2,2
gene	ESTs, Highly similar to putative Ras5-interacting protein (clone L1-57) [H.sapiens] (incyte PD:1984130)	1984130	2,2
gene	ESTs (incyte PD:1366043)	1366043	2,1
gene	ESTs, Weakly similar to III <sub>1</sub> ALU SUBFAMILY_J WARNING_ENTRY_III <sub>1</sub> [H.sapi]	2133481	2,1
gene	ensl (incyte PD:2133481)	2133481	2,1
gene	ESTs (incyte PD:1888670)	1888670	2,1
gene	ESTs (incyte PD:1349433)	1349433	2,1
gene	ESTs, Weakly similar to putative p150 [H.sapiens] (incyte PD:2936403)	2936403	2,1
gene	ESTs (incyte PD:414891)	414891	2,1
gene	ESTs (incyte PD:2060416)	2060416	2,1
gene	ESTs (incyte PD:3104921)	3104921	2,1
gene	ESTs (incyte PD:57997)	57997	2,1
gene	Not mapped (incyte PD:1464613)	1464613	2,1
gene	ESTs (incyte PD:1641775)	1641775	2,1
gene	Human clone 23933 mRNA sequence (incyte PD:2266572)	2266572	2,1
gene	amionide binding protein_1 (amine oxidase (copper-containing)) (incyte PD:3676190)	3676190	2,2

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gene	Human_guanine_nucleotide_exchange_factor_mRNA_complete cds (incyte_PD:1902190)	1962190	2,1
gene	ESTs (incyte_PD:2279230)	2279230	2,1
gene	ESTs (incyte_PD:3719865)	3719865	2,1
gene	preferentially expressed antigen of melanoma (incyte_PD:2007654)	2007654	2,1
gene	ESTs (incyte_PD:1302785)	1302785	2,1
gene	Homo sapiens_mRNA_from_chromosome_5q21-22_dome.FBR89 (incyte_PD:2501484)	2501484	2,1
gene	pancreatic_lipase-related protein_1 (incyte_PD:2084515)	2084515	2
gene	ESTs (incyte_PD:2691093)	2691093	2
gene	ESTs_Highly similar to PP2C [H.sapiens] (incyte_PD:2182353)	2182353	2
gene	surfactant_pulmonary-associated protein_B (incyte_PD:1988674)	1988674	2
gene	ESTs_Moderately similar to_III_ALU_SUBFAMILY_J_WARNING_ENTRY_III.H.sapiens] (incyte_PD:520342)	520342	2
gene	ESTs_Moderately similar to_III_ALU_SUBFAMILY_SQ_WARNING_ENTRY_III.H.sapiens] (incyte_PD:1849453)	1849453	2
gene	ESTs_Weakly similar to_(define_not_available_4587207)_H.sapiens] (incyte_PD:2296344)	2296344	2
gene	ESTs (incyte_PD:2317034)	2317034	2
gene	ESTs_Weakly similar to_III_ALU_SUBFAMILY_SB_WARNING_ENTRY_III.H.sapiens] (incyte_PD:1638184)	1638184	2
gene	ESTs (incyte_PD:1428856)	1428856	2
gene	ESTs (incyte_PD:3508727)	3508727	2
gene	ESTs_Weakly similar to_III_ALU_SUBFAMILY_J_WARNING_ENTRY_III.H.sapiens] (incyte_PD:1431969)	1431969	2
gene	Not mapped (incyte_PD:1393855)	1393855	2
gene	ESTs (incyte_PD:2045755)	2045755	2
gene	ESTs (incyte_PD:1686727)	1686727	2
gene	ESTs (incyte_PD:2344817)	2344817	2
gene	KIAA0335 gene product (incyte_PD:2308348)	2308348	2
gene	ESTs (incyte_PD:1417114)	1417114	2
gene	ESTs (incyte_PD:2459069)	2459069	2
gene	putative gene product (incyte_PD:1300530)	1300530	2
gene	breast cancer 2_early onset (incyte_PD:2468523)	2468523	2
gene	nucleolar autoantigen_(35kD)_similar_to_rat_synaptonemal_complex_protein (incyte_PD:81490)	81490	2

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gene	kinesin family member 5C [ncycle PD:159268]	159268	-2
gene	ESTs, highly similar to CDV-1R protein [Musculus] [ncycle PD:1494531]	1494531	-2
gene	ESTs [ncycle PD:2618859]	2618859	-2
gene	ESTs [ncycle PD:2286816]	2286816	-2
gene	activating transcription factor 4 (tax-responsive enhancer element 867) [ncycle PD:2916261]	2916261	-2
gene	ESTs [ncycle PD:1472206]	1472206	-2
gene	desmocollin 2 [ncycle PD:496003]	496003	-2
gene	Not mapped [ncycle PD:341263]	341263	-2
gene	ESTs [ncycle PD:1440279]	1440279	-2
gene	differentiated Embryo Chondrocyte expressed gene 1 [ncycle PD:1732479]	1732479	-2
gene	lectin, galactoside-binding, soluble, 3, (galactin-3) [ncycle PD:2921194]	2921194	-2
gene	cabinidin 1, (28kD) [ncycle PD:629769]	629769	-2
gene	serine protease inhibitor, Kazal type 1 [ncycle PD:2373608]	2373608	-2
gene	gogi, SNAP receptor complex member 2 [ncycle PD:3279439]	3279439	-2
gene	Rho-associated, coiled-coil containing protein kinase 1 [ncycle PD:1351711]	1351711	-2
gene	plectin 1, intermediate filament binding protein, 500kD [ncycle PD:1907232]	1907232	-2
gene	ESTs, Weakly similar to DAP-1 beta [H.sapiens] [ncycle PD:2902846]	2902846	-2
gene	actinin, alpha 4 [ncycle PD:1597330]	1597330	-2
gene	ubiquitin-activating enzyme E1 (A1S9T and BN75 temperature sensitivity complementing) [ncycle PD:1674422]	1674422	-2
gene	apoptosis inhibitor 3 [ncycle PD:2912879]	2912879	-2
gene	Human mRNA for unknown product, partial cds [ncycle PD:1402715]	1402715	-2
gene	ESTs, Highly similar to DIAMINE ACETYLTRANSFERASE [H.sapiens] [ncycle PD:63038]	63038	-2
gene	ESTs [ncycle PD:1912294]	1912294	-2
gene	Human autoantigen mRNA, complete cds [ncycle PD:3374419]	3374419	-2
gene	ESTs [ncycle PD:565269]	565269	-2
gene	hect (homologous to the E6-AP [UBE3A] carboxyl terminus) domain and ROC1 (CHC1)-like domain (RLD) 1 [ncycle PD:4292515]	4292515	-2
gene	phospholipase, glycoconjugate, muscle (McArdle syndrome, glycogen storage disease type VI) [ncycle PD:2635543]	2635543	-2
gene	KIAA0336, gene product [ncycle PD:3520448]	3520448	-2

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gene	Homo sapiens SOX22 protein (SOX22) mRNA, complete cds (lncyte_PD:2824870)	-2.1
gene	Homo sapiens beta III spectrin (SPTBN2) mRNA, partial cds (lncyte_PD:3432208)	-2.1
gene	ESTs, Weakly similar to (define_not_available_4929591) [H.sapiens] (lncyte_PD:3596244)	-2.1
gene	ubiquitin specific protease 5 (isopeptidase T) (lncyte_PD:2493777)	-2.1
gene	Homo sapiens mRNA for KIAA0841 protein, partial cds (lncyte_PD:3971091)	-2.1
gene	laminin, alpha 3 (lncin_150KD), kalinin (165KD), BM600 (150KD), epiligrin (lncyte_PD:1818527)	-2.1
gene	Human mRNA for KIAA0185 gene, partial cds (lncyte_PD:2503208)	-2.1
gene	desmoplakin (DPI, DPIP) (lncyte_PD:179929)	-2.1
gene	Cyclin-dependent kinase inhibitor 1A (p21, Cip1) (lncyte_PD:1804548)	-2.1 p21
gene	alpha thalassemia/mental retardation syndrome X-linked (lncyte_PD:4106629)	-2.2
gene	phosphatidylinositol-4-phosphate 5-kinase, type II, beta (lncyte_PD:1315666)	-2.2
gene	ARF1 (adfin-related protein 1, yeast) homolog A (centractin, alpha) (lncyte_PD:1841462)	-2.2
gene	Keratin 7 (lncyte_PD:1649959)	-2.2
gene	Homo sapiens mRNA for 6-phosphofructo-2-kinase (fructose-2, 6-bisphosphatase, complete cds (lncyte_PD:1302221)	-2.2
gene	ESTs (lncyte_PD:8552)	-2.2
gene	vav 2 oncogene (lncyte_PD:3744592)	-2.3
gene	epithelial membrane protein 1 (lncyte_PD:1624024)	-2.3
gene	ESTs (lncyte_PD:2129939)	-2.3
gene	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (lncyte_PD:179598)	-2.3
gene	insulin-like growth factor 1 receptor (lncyte_PD:2587262)	-2.3
gene	protein kinase C substrate 80K-H (lncyte_PD:1723971)	-2.3
gene	guanylate binding protein 2, interferon-inducible (lncyte_PD:1610993)	-2.3
gene	interferon, gamma-inducible protein 16 (lncyte_PD:2508261)	-2.3
gene	N-myc downstream regulated (lncyte_PD:2055569)	-2.3
gene	ESTs (lncyte_PD:3971258)	-2.4
gene	Homo sapiens transcriptional enhancer factor 1 (TEF1) DNA, complete CDS (lncyte_PD:2857175)	-2.4
gene	protein tyrosine phosphatase, receptor type, J (lncyte_PD:3818113)	-2.4
gene	Human cleavage signal 1 protein, mRNA, complete cds (lncyte_PD:2054053)	-2.4

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gene	ESTs_(lncocyte_PD:187276)		187276	-2.4
gene	hypothetical protein of unknown function_(lncyte_PD:1402462)		1402462	-2.5
gene	Human mRNA for KIAA0068 gene, partial cds_(lncyte_PD:3042837)		3042837	-2.5
gene	BMX non-receptor tyrosine kinase_(lncyte_PD:1655995)		1655995	-2.5
gene	nel (chicken)-like 2_(lncyte_PD:2285502)		2285502	-2.5
gene	homolog of Drosophila past_(lncyte_PD:1336738)		1336738	-2.5
gene	ESTs_(lncyte_PD:1382947)		1382947	-2.5
gene	ESTs_(lncyte_PD:1967531)		1967531	-2.5
gene	ESTs_(lncyte_PD:2369022)		2369022	-2.5
gene	cannabinoid_receptor_1_(brain)_(lncyte_PD:112853)		112853	
gene	keratin_hair_baslc_1_(lncyte_PD:1919158)		1919158	-2.6
gene	S100 calcium-binding protein A4_(calcium_protein_calvasculin_melanastatin_murine_placental_homolog)_(lncyte_PD:1222317)		1222317	-2.6
gene	fibroblast activation protein_alpha_(lncyte_PD:2483605)		2483605	-2.6
gene	Homo sapiens KIAA0421 mRNA, partial cds_(lncyte_PD:4253663)		4253663	-2.6
gene	Not mapped_(lncyte_PD:2204871)		2204871	-2.7
gene	lamin B2_(lncyte_PD:2414632)		2414632	-2.7
gene	KIAA0138 gene product_(lncyte_PD:1731569)		1731569	-2.7
gene	H.sapiens mRNA for protein-tyrosine-phosphatase D1_(lncyte_PD:2605804)		2605804	-2.7
gene	axonal transport of synaptic vesicles_(lncyte_PD:3856893)		3856893	-2.7
gene	Homo sapiens miRNA; cDNA DKFp566F0219_(from clone DKFp566F0219)_(lncyte_PD:220566)		220566	-2.8
gene	nuclear factor_1C_(CCAAAT-binding_transcription_factor)_(lncyte_PD:1670221)		1670221	-2.8
gene	ESTs_(lncyte_PD:1540157)		1540157	-2.8
gene	514-oncocal trophoblast_glycoprotein_(lncyte_PD:1283532)		1283532	-2.8
gene	glucose-6-phosphatase_catalytic_(glycogen_storage_disease_type_1_von_Gierke_disease)_(lncyte_PD:4287327)		4287327	-2.8
gene	Interleukin_6_signal_transducer_(gp130_oncostatin_M_receptor)_(lncyte_PD:2172334)		2172334	-2.8
gene	hydroxyprostaglandin_dehydrogenase_15_(NAD)_(lncyte_PD:1578941)		1578941	-2.8
gene	v-myb avian myeloblastosis viral oncogene homolog-like 2_(lncyte_PD:494905)		494905	-2.9

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gene	Homo sapiens Nedd4-like ubiquitin-protein ligase YWIP2 mRNA, complete cds (Incyte PD:869818)	869818	-2.9
gene	UDF-Galactose-4-epimerase, beta, 14-galactosyltransferase, polypeptide 1 (Incyte PD:1736926)	1736926	-3
gene	Human mRNA for KIAA0220 gene, partial cds (Incyte PD:2657738)	2657738	-3
gene	Human mRNA for KIAA0220 gene, partial cds (Incyte PD:2657738)	2657738	-3
gene	Salting factor, arginine/leucine-rich 8 (Incyte PD:1728574)	1728574	-3
gene	Interleukin enhancer binding factor 3, 90kD (Incyte PD:1674263)	1674263	-3.1
gene	ESTs (Incyte PD:1635954)	1635954	-3.2
gene	regulator of G-protein signalling 4 (Incyte PD:617517)	617517	-3.3
gene	eukaryotic translation initiation factor 4 gamma, 1 (Incyte PD:1965695)	1965695	-3.4
gene	REMOVED FROM DATABASE (Incyte PD:85246)	85246	-3.4
gene	zinc finger protein 162 (Incyte PD:2655068)	2655068	-3.5
gene	Homo sapiens TIF-1 interacting peptide 5 mRNA, partial cds (Incyte PD:4251662)	4251662	-3.7
gene	Homo sapiens ataxin-2-like protein A2LP (A2LG) mRNA, complete cds (Incyte PD:1712724)	1712724	-3.7
gene	quiescin Q6 (Incyte PD:1854220)	1854220	-3.8
gene	Human transporter protein (g17) mRNA, complete cds (Incyte PD:86661)	86661	-3.9
gene	nuclear mitotic apparatus protein 1 (Incyte PD:2700234)	2700234	-3.9
gene	ytliac (Incyte PD:3868809)	3868809	-4.1
gene	myosin, heavy polypeptide 11, smooth muscle (Incyte PD:1866751)	1866751	-4.1
gene	cut (Drosophila)-like 1 (CCAAT displacement protein) (Incyte PD:2317648)	2317648	-4.1
gene	filamin A, alpha (actin-binding protein-280) (Incyte PD:1708528)	1708528	-4.2
gene	nucleoporin 98kD (Incyte PD:1611933)	1611933	-4.2
gene	ESTs, Highly similar to (define not available_3866200) (Incyte PD:1554358)	1554358	-4.4
gene	Human mRNA for KIAA0194 gene, partial cds (Incyte PD:1429306)	1429306	-4.5
gene	microtubule-associated protein 4 (Incyte PD:2992994)	2992994	-4.6
gene	U5 snRNP-specific protein (220 kD), ortholog of S. cerevisiae Prp8 (Incyte PD:3616229)	3616229	-4.7
gene	ser-Thr protein kinase related to the myotonic dystrophy protein kinase (Incyte PD:1602261)	1602261	-4.8
gene	nect domain and RLD 2 (Incyte PD:2739109)	2739109	-4.9
gene	KIAA0018 gene product (Incyte PD:2962167)	2962167	-4.9

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gene	laminin_gamma_1 (formerly LAMB2) (Incyte PD:159344)	1599344	-4.9
gene	Not mapped (Incyte PD:3427594)	3427594	-5.5
gene	protein phosphatase 1, regulatory subunit 10 (Incyte PD:2314555)	2314555	-5.7
gene	general transcription factor IIIC, polypeptide 1 (alpha subunit_220KD) (Incyte PD:486304)	486304	-6.7
gene	EST's_Highly_similar_to_RanTC4-binding_nucleopora_protein [H.sapiens] (Incyte PD:3030988)	3030988	-7
gene	Homo sapiens mRNA for KIAA0911 protein, complete cds (Incyte PD:2578710)	2578710	-7.4
gene	vaiy-4RNA_synthetase_1 (Incyte PD:1829709)	1829709	-28

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[illegible]

AA053060	RKEN_CDNA_214124.UT_gene	1.5	1.6	1.1	2.4	1.35143*	-1.3	1.8	1.74297*	1.7	1.4	2.0	1.3
AA071412	ESTs	1.4	1.4	-4.2	2.3	4.7	-1.01971**	1.3	1.8	1.2	1.3	1.6	1.6
AA054606	bats specific gene A2	1.1	-1.5	1.2	1.6	1.3	1.6071*	-1.6	-1.0	1.3	1.1	1.4	1.3
AA073925	ESTs	1.3	1.6	-1.4	2.5	2.0	-1.1707**	1.1	1.3	1.6	1.2	1.6	1.3
AA100416	ESTs_Moderately similar to 5'-ACT_1_FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN, PEROXISOMAL	1.6	1.6	1.5	1.5	1.1	-1.11723*	-1.8	-1.0	1.3	1.1	1.2	1.4
AB022196	RKEN_CDNA_580459B16.5_gene	1.0	-1.3	1.1	1.6	1.3	2.1	-1.8	-1.0	1.5	1.2	1.2	1.9
AA066416	RKEN_CDNA_279247C29_gene	-1.1	-1.5	-2.2	1.2	-1.0	1.26303**	-1.1	-1.2	1.2	1.2	1.2	1.6
AA161648	gallinacea type II	-1.1	1.0	-1.2	-1.1	-1.2	1.24634**	-1.8	1.1	1.0	1.2	1.1	1.3
W12636	ginsenos A10	1.9	-1.7	-1.1	-2.3	4.5	-1.06667*	-1.3	-1.1	1.1	-1.0	1.0	-1.9
AA072907	transcript 2, beta-3a, embryonic chain	-1.5	-1.5	1.1	-1.8	-1.4	-1.20487*	1.7	-1.2	-1.4	1.1	-2.7	-1.9
AA163006	ESTs_Nearly similar to N1C1_MOUSE_NEUROGENIC LOCUS, NOTCH HOMOLOG, PROTEIN, L_PHEC	-1.3	-1.3	-1.0	1.1	1.2	1.76693**	-1.2	-1.2	-1.5	-1.3	-1.7	-1.9
AA172581	ESTs	-	-	-	1.33228	-	-	-	-	-	-	-	-
AA172581	ESTs	1.25704**	1.37307*	1.03756*	-1.0	1.4912**	-1.2	-1.1781*	-1.3	-1.2	-1.1	-1.9	-
AA040744	RKEN_CDNA_270009C18_gene	-1.4	-1.3	-1.5	-2.2	-1.0	-1.4	-1.1	-1.4	-1.4	-1.3	-1.3	-1.9
AA111016	gH2a2a_1	1.2066*	1.63915*	1.19323*	1.10085	1.61546*	1.67671**	-1.26583*	1.20291*	1.04301*	-1.3	-1.1	-1.9
AA075111	RKEN_CDNA_181007A24_gene	1.4	1.3	-1.0	-2.1	-1.0	-1.5	1.0	-1.4	-2.2	-1.2	-1.2	-2.0
AA068763	hemoglobin, beta adult major chain	1.3	-1.2	1.4	-4.0	1.1	-4.2	3.9	-1.1	-1.3	1.5	-1.8	-2.0
AA100071	hemoglobin, beta adult major chain	1.3	-1.4	1.2	-3.0	-1.1	4.3	3.2	1.1	-1.3	1.8	-1.7	-2.0
AA040305	RKEN_CDNA_130014P09_gene	-1.2	-1.2	-1.1	-1.1	-1.0	1.26358**	-1.5	-1.4	-1.1	-1.3	-1.2	-2.1
AA171648	ESTs	1.18694**	1.40956*	1.07383**	-1.2	1.1	1.63944**	1.07811*	1.49991**	1.3	-	1.16867*	-1.3
AA053939	RKEN_CDNA_221414L06_gene	-1.8	-1.8	-1.4	-3.1	-1.9	1.1	-1.5	-2.0	-1.6	-2.1	-1.6	-2.1
AA165847	ESTs	-1.0	-1.0	1.24928*	1.05247**	1.1	-1.45624**	-1.6	1.30266*	1.44776*	-1.3	1.2	2.2
1H41372	isoaccepting protein, ribosomal	1.2	-1.1	-1.0	-1.1	1.0	1.06938**	-1.1	-1.8	1.1	-1.1	-2.2	-2.1
AA162834	immunoglobulin heavy chain, 1 (gamma 1G2b)	1.0	1.1	1.6226*	-1.0	1.1	1.18442**	-1.41372**	1.1	-1.1	1.2	1.1	-2.2
AA162834	immunoglobulin heavy chain, 1 (gamma 1G2b)	1.1	-1.1	1.5	-1.1	-1.1	-1.36935*	1.2	-3.1	1.1	1.4	-1.6	-2.2

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AA057624, angiotensin vasopressin	1.4	-1.6	-1.2	-1.1	-1.9	-2.7	-2.0	-1.4	-1.3	1.4	-1.2	-2.3
AA058305, orthosialosyl binding globulin	1.0	1.2	1.5	-1.1	1.2	1.4	-2.4	-2.3	1.1	-1.0	-1.3	-2.4
AA132655, RCN1, CDNA_210300/524, gene	-1.1	-2.2	-1.5	-1.2	-1.0	-1.9	-1.1	1.1	-1.3	-1.0	-1.0	-2.4
AA152410, immunoglobulin kappa chain variable 2B (V2B)	1.3	-1.6	-1.5	-1.0	-2.1	-3.1	-2.2	-1.3	-1.3	1.6	-1.1	-2.5
AA02101, EST1_WashU, Jnt1E_p1, COB4_HUMAN, COMPLEMENT COMPONENT_10, ALPHA_CHAIN, PRECURSOR C_10 (S-sense)	2.7	-1.7	2.2	-1.0	1.1	5.0 (28)	1.9	20.2	-1.5	-1.3	-1.4	-2.7
AA049194, immunoglobulin kappa chain variable 2D (V2D family)	1.4	-1.2	-1.4	-1.1	-1.9	-2.9	-2.6	-1.6	-1.0	1.4	-1.0	-2.7
AA092560, serum albumin, variant	2.9	-1.7	2.0	1.1	-1.1	1.6 (54)	-1.3	-22.1	-1.4	-1.5	-1.3	-2.9
AA159823, immunoglobulin heavy chain_3, (sensus) (527b)	-1.0	-1.6	-1.0	1.5	1.5	-2.5 (20)	1.2	1.2	1.4	-1.0	1.2	-3.4

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TABLE 2

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placenta/uterus	spl	panc	liv	stom	int	col	br	lung	blad	kidn	plut	main
AA61882 EST	1.5	1.2	1.0	1.4	4.937+	1.00000+	1.5	2.3102+	2.00474+	1.5	2.5	2.0
AA64926 RIKEN cDNA 161041E09, 161041E09	1.8	1.9	-1.3	2.6	1.6	1.01540+	1.1	2.2	2.1	1.6	2.5	2.3
AA70585 perababun	-1.1	-1.4	-1.4	1.4	1.3	2.0	1.5	1.2	1.1	1.2	2.5	-1.2
AA46930 choline kinase	1.7	1.5	-1.4	1.1	2.0	1.31540+	1.3	2.3	2.0	1.5	2.2	2.1
AA47387 ESTs	1.1	1.7	1.057+	2.1	1.65834+	1.00081+	2.8	1.6	1.7	1.8	2.1	2.1
AA75492, steryl-Coenzyme A desaturase 1	-1.1	-1.1	-1.4	1.8	1.4	1.50786+	1.1	-1.2	-1.0	-1.2	2.1	-1.8
AA14413, 3'-phosphoadenine 5'-phosphosulfate synthase 2	1.2	-1.2	1.5	1.2	3.7	-1.4	-1.3	1.4	1.5	1.3	-2.1	-1.7
AA53202 ribosomal protein S6	1.5	1.5	1.0	-2.3	1.2	-1.20693+	1.6	1.6	1.6	1.4	2.1	1.7
AA78937 carboxyl ester lipase	1.5	1.8	-1.4	-2.3	-8.9	-1.9	-1.3	-1.4	-1.1	1.1	2.0	2.2
AA54443, glyoxysomal dehydrogenase	1.2	1.5	1.0	3.2	1.7	1.2437+	1.4	1.3	1.7	1.4	2.0	1.7
AA37349 transition protein 1	-1.1	1.2	-1.2	2.1	1.4	-2.3	-1.0	1.6	1.2	1.2	2.0	1.8
AA50586 RIKEN cDNA 161010M01, gene	1.1	1.4	-1.2	1.4	1.6	-1.0	-1.1	1.6	1.2	1.2	2.0	2.1551+
AA47566 ESTs, Moderately similar to alias D1C1 (H. sapiens)	1.3	1.5	1.2	2.0	1.9	-1.305+	1.5504+	1.6	1.4	1.4	2.0	1.9
AA25260 RIKEN cDNA 241024L17, gene	1.5	1.5	1.1	2.4	1.39143+	-1.3	1.8	1.7	1.7	1.4	2.0	1.9
AA65875, different-related cryptin 6	-1.2	1.1	-1.2	1.1	1.6	1.7	2.6	1.3	1.5	1.1	1.0	1.5
AA65897 ESTs	1.1	1.8	-1.5	2.6	1.7	1.17361+	2.5	1.35884+	1.7	1.4	1.9	2.1
AA152031, Public domain EST	1.26489+	1.12314+	-1.10079+	2.07733+	1.43304+	-1.26463+	1.9585+	1.48424+	1.36886+	1.49743+	1.5	1.2
AA517065 T-box 15	1.3	1.6	1.0	2.3	1.7	-1.58578+	1.3	1.6	2.0	1.5	1.6	1.8
AA51769 ESTs	1.3	1.8	-1.2	2.1	1.32145+	-1.2	1.6	1.6	1.7	1.5	1.6	1.5
AA07692 ESTs	1.3	1.8	-1.4	2.2	2.0	1.20707+	1.1	1.6	1.9	1.2	1.8	1.9
AA475826, acetyltransferase	-1.0	1.6	-1.3	1.3	1.5	-1.2	1.4	1.1	1.1	1.2	1.8	-1.1
AA476874, ATPase, H <sup>+</sup> -transporting, lysosomal (yeast) (yeast) (pump) 49KD	-1.5	1.4	1.3	1.0	1.4	1.8	-1.1	-1.9	-1.5	-1.0	-1.9	-1.2
AA475847, non-catalytic region of lysosomal kinase adaptor protein 2	-1.8	1.1	1.3	1.0	1.2	1.4	-2.2	-2.2	-1.8	-1.3	-1.9	-1.2
AA5474, metallothionein 2	-1.2	-2.2	2.1	1.2	1.2	1.4	-2.2	-2.2	-1.8	-1.3	-1.9	-1.0
AA67674, S-phase kinase-associated protein 2 (hsp)	-1.8	-1.2	2.0	1.5	1.2	2.74757+	-1.73102+	-2.2	-1.8	-1.4	-1.9	-1.3
AA63765 metallothionein 1	1.0	1.1	2.5	1.2	2.4	1.5	1.2	-1.8	-1.3	1.6	-1.9	-1.2
AA60886, not related transcription factor 3	-2.0	1.1	1.2	1.4	1.4	1.82264+	-1.76783+	-2.0	-1.6	-1.3	-1.9	-1.0
AA21632, small inducible cyclase A6	1.0	-1.0	1.6	-1.6	1.3	-1.2	-1.3	1.2	1.3	1.1	-1.9	-1.7
AA681320, actin receptor interacting protein 1	-1.9	1.4	1.3	1.3	1.5	2.64444+	1.0	-2.7	-1.4	-1.1	-1.9	-1.3
AA25503, axoninogenin E	1.2	1.3	1.6	-1.7	1.5	-1.0	1.6	-1.9	-1.3	-1.5	-2.0	-1.2
AA622116, gonadotropin	-1.1	-1.1	1.5	-1.5	-1.4	1.65627+	-1.3	-1.7	-1.0	1.1	-2.0	-1.6

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TABLE 2



AA059341	ESTs	-12	13	22	15	16	123416	10	20	-4	-13	-20	10
AA056016	Riken cDNA, 118002H23 gene	-16	12	11	15	12	133219	-20	-24	-14	-18	-20	-13
AA176276	small nuclear protein, X-linked	-17	-14	11	16	12	16	-6	-25	-16	-12	-20	-15
AA067372	Riken cDNA, 110017F10 gene	-13	11	14	11	-10	150739	-10	-18	-19	-13	-20	-16
AA343383	Riken cDNA, 120018J05 gene	-16	10	14	14	13	243037	-14	-20	-17	-11	-20	-13
AA049767	interleukin (SH3 domain protein 1A)	-16	10	11	20	15	250774	-10	-18	-15	-12	-11	-12
AA071983	topoisomerase (DNA) III, beta	-17	-10	14	11	11	21785	-14	-25	-17	-15	-21	-15
AA071168	sarcoplasmic	-14	12	14	14	14	275327	-12	-18	-14	-12	-21	-14
AA013726	cellulopis J	-10	-10	-12	26	13	14	-12	16	12	11	-21	15
AA028661	ESTs	-26	-11	10	-14	12	12	-16	-28	-21	-17	-22	-18
AA048650	Public domain EST	-15	-10	15	12	12	150639	-15	-22	-11	-12	-22	-11
AA339432	alpha leoprotein	-11	-18	-11	-13	-14	-13	-13	-15	-10	-13	-22	-18
W56707	ESTs	-12	14	21	17	16	18	11	-26	-14	-14	-23	-11
AA024717	Public domain EST	-25	18	20	12	23	22	-10	-42	-18	-12	-23	11
AA047436	synaptotagmin complex, protein 3	-12	26	14	13	13	274133	-11	-37	-21	-14	-23	-13
AA045243	hemoglobin Y, beta-like embryonic chain	-14	-16	11	-12	-11	13	-17	-18	-13	-10	-23	-15
AA071929	ESTs, Weakly similar to zinc finger protein_95 (Mus musculus)	-24	12	13	12	12	11716	-20	33	-22	-14	-24	-14
AA027268	actinin, 8	-11	-12	-11	14	14	-28	12	10	10	12	-24	13
AA045635	cell division cycle 2 homolog (S. pombe)-like 2	-11	-11	13	14	11	23	-15	-30	-23	-15	-24	-14
AA074101	luciferase-associated calcium signal transducer 2	-26	-11	15	13	12	6591	-17	-21	-15	-15	-24	-12
AA037388	ESTs, Weakly similar to ORF2 (Mus musculus)	-18	14	12	-10	14	18	-14	-13	-17	-15	-24	-12
AA022288	actinoprotein A1	-18	-15	11	-24	24	24	-19	-30	-12	-21	-25	-16
AA041478	DNA fragment, CHY 7, ERATO Dcl 485, overexpressed	-17	12	14	12	12	230644	-10	-20	-14	-11	-25	-12
AA178045	DNA fragment, CHY 7, ERATO Dcl 485, overexpressed	-25	11	14	14	11	37	-17	-30	-23	-16	-25	-11
AA034678	nuclein	-23	10	12	-10	12	24	-13	-25	-21	-14	-28	-14
AA028707	hemoglobin Z, beta-like embryonic chain	-15	-15	11	-18	-14	180497	-17	-12	-14	11	-27	-18
AA045177	tumor-suppressing, subchromosomal transferable fragment 3	-21	11	19	-12	11	25221	-18	-30	-21	-18	-29	-10
AA076520	ADP-ribosylarginine hydrolase	10	-11	12	11	-11	124040	-11	11	10	33	-10	10
AA168966	ESTs	-32	14	15	15	13	17357	-13	56	-10	-38	-39	-14
AA049985	hemoglobin X, alpha-like embryonic chain (H. faba complex)	11	-16	-13	-12	-22	112322	-21	-20	-10	-12	-40	-19

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kidney	sp1	panc	liv	stom	int	col	br	lung	blad	kid	plut	mam
Description	PL 45 BDmean 25 BDmean	PL 45 BDmean 25 BDmean	PL 45 BDmean 25 BDmean	PL 45 BDmean 25 BDmean	PL 45 BDmean 25 BDmean	PL 45 BDmean 25 BDmean	PL 45 BDmean 25 BDmean	PL 45 BDmean 25 BDmean	PL 45 BDmean 25 BDmean	PL 45 BDmean 25 BDmean	PL 45 BDmean 25 BDmean	PL 45 BDmean 25 BDmean
AA762407 EST1	-1.07330+ -1.41617+	-1.23897+ -1.41617+	-1.23897+ -1.41617+	1.12201+ -1.32665+	-1.32665+ -1.61984+	-1.61984+ -1.32648+	-1.32648+ -1.24845+	-1.24845+ -1.32648+	-1.32648+ -1.24845+	-1.32648+ -1.24845+	-1.32648+ -1.24845+	-1.32648+ -1.24845+
AA81891 Mus musculus, clone MGC-5721, mRNA, complete cds	-1.1 -2.0	-1.1 -2.0	-1.1 -2.0	1.0 -1.8	1.0 -1.8	1.0 -1.8	-2.3 -1.5	-2.4 -1.4	-2.4 -1.4	-2.4 -1.4	-2.4 -1.4	-2.4 -1.4
AA760002 beta-2-microglobulin (beta2m)	-1.2 -1.1	-1.2 -1.1	-1.2 -1.1	-1.1 -1.1	-1.1 -1.1	-1.1 -1.1	1.4 -1.4	1.1 -1.1	1.1 -1.1	1.1 -1.1	1.1 -1.1	1.1 -1.1
AA106125 cytochrome P450, 2B4	1.3 -1.3	1.3 -1.3	1.3 -1.3	1.3 -1.3	1.4 -1.4	1.4 -1.4	1.0 -2.4	1.3 -1.3	1.1 -2.3	1.1 -2.3	1.1 -2.3	1.1 -2.3
AA158437 Mus musculus, Zolpich-HSD, mRNA, Inv. 20alpha-hydroxysteroid dehydrogenase, complete cds	1.3 -1.5	1.3 -1.5	1.3 -1.5	1.1 -1.2	1.1 -1.2	1.1 -1.2	-1.2 -1.1	-1.2 -1.1	-1.2 -1.1	-1.2 -1.1	-1.2 -1.1	-1.2 -1.1
AA14454 reduced in osteoclasts transporter	-1.1 -1.1	-1.1 -1.1	-1.1 -1.1	1.0 -1.0	1.0 -1.0	1.0 -1.0	-1.2 -1.2	-1.2 -1.2	-1.2 -1.2	-1.2 -1.2	-1.2 -1.2	-1.2 -1.2
AA21197 myoglobin	-1.0 -2.5	-1.0 -2.5	-1.0 -2.5	1.0 -1.1	1.0 -1.1	1.0 -1.1	-1.2 -1.7	-1.7 -4.3	-1.7 -4.3	-1.7 -4.3	-1.7 -4.3	-1.7 -4.3
W18039 glutathione S-transferase omega 1	1.2 -1.1	1.2 -1.1	1.2 -1.1	1.4 -1.4	1.4 -1.4	1.4 -1.4	1.2 -1.2	1.2 -1.2	1.4 -1.4	1.4 -1.4	1.4 -1.4	1.4 -1.4
AA87417 cytochrome P450, 2B4	1.2 -1.6	1.2 -1.6	1.2 -1.6	1.1 -1.1	1.1 -1.1	1.1 -1.1	-2.1 -1.2	-2.1 -1.2	-2.1 -1.2	-2.1 -1.2	-2.1 -1.2	-2.1 -1.2
AA807441 RKEN cDNA 081001/1104 gene	1.2 -1.1	1.2 -1.1	1.2 -1.1	1.3 -1.3	1.3 -1.3	1.3 -1.3	-1.1 -1.487+	-1.1 -1.487+	-1.1 -1.487+	-1.1 -1.487+	-1.1 -1.487+	-1.1 -1.487+
AA148478 M. musculus mRNA (BC10) for I-gA V-D-heavy chain	-1.3 -1.0	-1.3 -1.0	-1.3 -1.0	-1.6 -2.7	-2.0 -2.4	-2.0 -2.4	-1.1 -1.4	-1.1 -1.4	-1.1 -1.4	-1.1 -1.4	-1.1 -1.4	-1.1 -1.4
AA08815 Public domain EST	1.2 -1.3	1.2 -1.3	1.2 -1.3	1.2 -1.2	1.2 -1.2	1.2 -1.2	-1.8 -1.2	-1.8 -1.2	-1.8 -1.2	-1.8 -1.2	-1.8 -1.2	-1.8 -1.2
AA145454 insulin-like growth factor binding protein 4	1.0 -1.5	1.0 -1.5	1.0 -1.5	1.3 -1.2	1.3 -1.2	1.3 -1.2	1.0 -1.1	1.0 -1.1	1.0 -1.1	1.0 -1.1	1.0 -1.1	1.0 -1.1
AA04866 ESTs	1.35481+ 1.65119+	1.35481+ 1.65119+	1.35481+ 1.65119+	1.04663+ 2.2165167+	1.04663+ 2.2165167+	1.04663+ 2.2165167+	1.07014+ 1.61678+	1.07014+ 1.61678+	1.07014+ 1.61678+	1.07014+ 1.61678+	1.07014+ 1.61678+	1.07014+ 1.61678+
AA108417 insulin-like growth factor binding protein 4	-1.0 -1.5	-1.0 -1.5	-1.0 -1.5	1.2 -1.2	-1.1 -1.1	-1.1 -1.1	-1.3 -1.0	-1.2 -1.2	-1.2 -1.2	-1.2 -1.2	-1.2 -1.2	-1.2 -1.2
AA450534 glutamine synthetase, pseudogene, 1	1.1 -1.1	1.1 -1.1	1.1 -1.1	1.2 -1.4	1.2 -1.4	1.2 -1.4	1.4 -1.3	1.4 -1.3	1.4 -1.3	1.4 -1.3	1.4 -1.3	1.4 -1.3
AA52959 ESTs	-1.3 -1.1	-1.3 -1.1	-1.3 -1.1	-1.2 -1.2	-1.1 -1.1	-1.1 -1.1	1.2 -1.1	1.2 -1.1	1.2 -1.1	1.2 -1.1	1.2 -1.1	1.2 -1.1
AA520138 RKEN cDNA 330240/1819 gene	-1.4 -1.4	-1.4 -1.4	-1.4 -1.4	-1.1 -2.0	-1.1 -2.0	-1.1 -2.0	-2.1 -1.3	-2.1 -1.3	-2.1 -1.3	-2.1 -1.3	-2.1 -1.3	-2.1 -1.3
AA61008 ESTs	-1.13803+ -1.31577+	-1.13803+ -1.31577+	-1.13803+ -1.31577+	1.02390+ 1.06627+	1.02390+ 1.06627+	1.02390+ 1.06627+	-1.09915+ 1.35085+	-1.09915+ 1.35085+	-1.09915+ 1.35085+	-1.09915+ 1.35085+	-1.09915+ 1.35085+	-1.09915+ 1.35085+
AA355497 reelin binding protein 2, cellular	-2.0 -2.1	-2.0 -2.1	-2.0 -2.1	-1.6 -1.0	-1.6 -1.0	-1.6 -1.0	-1.3 -1.8	-1.3 -1.8	-1.3 -1.8	-1.3 -1.8	-1.3 -1.8	-1.3 -1.8
AA040322 tubulin factor 2, liposomally protein, 1	-1.1 -1.6	-1.1 -1.6	-1.1 -1.6	-1.2 -2.0	-1.2 -2.0	-1.2 -2.0	-1.4 -1.4	-1.4 -1.4	-1.4 -1.4	-1.4 -1.4	-1.4 -1.4	-1.4 -1.4
AA597097 Public domain EST	1.3 -1.9	1.3 -1.9	1.3 -1.9	-1.1 -1.0	-1.1 -1.0	-1.1 -1.0	1.2 -1.2	1.2 -1.2	1.2 -1.2	1.2 -1.2	1.2 -1.2	1.2 -1.2

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A036469 cyclin G	-1.2	1.0	1.3	-1.9	-1.8	-2.26973	1.2	-1.4	-1.4	-2.0	-1.0	-1.1
A095510 cathepin_13	-1.2	-1.6	-1.0	1.2	-1.5	-1.6	-1.1	1.1	-1.6	-2.1	-1.2	-1.0
A1530309 RIKEN cDNA 2210410L05 gene	-1.6	-1.6	-1.4	-2.1	-1.6	1.1	-1.5	-2.0	-1.6	-2.1	-1.6	-2.1
A4322006 apolipoprotein A-I	-1.9	-1.5	1.1	-2.4	2.4	2.4	-1.6	-6.0	-1.2	-2.1	-2.6	-1.6
A4684191 CDC-like kinase	1.5	-2.1	-1.5	-1.1	-2.0	-1.4	-1.5	-1.3	1.4	-2.1	1.4	1.2
A4322105 major urinary protein 1	-1.1	-2.4	-2.87649*	-7.8	-1.1	1.43224	-1.3	-7.1	-1.6	-2.2	-1.1	-1.2
A4434680 ESTs	-1.1	-1.1	-1.0	-1.0	-1.7	1.2	-1.0	-1.0	-1.1	-2.2	-1.0	-1.2
A4103485 deoxyribonuclease I	1.1	-1.6	-1.1	1.2	1.4	2.1	-2.3	-1.2	1.7	-2.4	1.3	-1.6
AA184421 ESTs	-1.1	1.0	-1.0	1.0	-1.4	1.1	1.4	1.2	-1.3	-2.4	-1.1	-1.1
AA060800 RIKEN cDNA 1700023M09 gene	-1.1	-1.8	-1.1	1.4	-1.5	1.6	-1.3	1.1	-1.7	-2.7	-1.1	1.1

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TABLE 2

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TABLE 2

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AA47439 synaptonemal complex protein 3	-2.8	1.2	2.8	1.4	1.5	2.74133	1.1	-3.7	-2.1	-1.4	-2.3	-1.3
AA67135 myosin heavy chain, cardiac muscle, adult	-1.1	-1.7	1.3	1.2	1.1	2.1	-1.9	-1.3	-2.1	1.4	-1.2	-1.3
AA77024 tropomyosin T3, skeletal, fast	1.4	-1.5	1.1	1.2	1.0	1.7	1.8	-1.1	-2.1	1.0	1.2	-1.2
AA70478 troponin	-2.3	1.0	1.2	-1.0	1.2	2.4	-1.3	-2.5	-2.1	-1.4	2.6	-1.4
AA42601 ESTs	-2.9	1.1	1.0	1.4	1.2	1.2	-1.8	-2.6	-2.1	-1.7	-2.2	-1.5
AA04127 tumor-suppressing subchromosomal transmissible fragment 3	-2.1	1.1	1.8	-1.2	1.1	2.03225	-1.8	-3.0	-2.1	-1.8	-2.0	-1.0
AA67301 tropomyosin T1, cardiac	1.4	-1.0	-1.1	-2.1	1.3	1.41297	-2.0	-2.0	-2.2	2.0	-1.0	1.3
AA67311 RIKEN cDNA 181007424, gene	1.4	1.3	1.0	-2.1	-14.0	-1.5	1.0	-1.4	-2.2	-1.2	-1.2	-2.0
AA77720 ESTs, Weekly similar to zinc finger protein 95 (M. musculus)	-2.4	1.2	1.3	1.2	1.2	1.7416	2.0	-3.3	-2.2	-1.4	-2.4	-1.4
AA61368 ESTs	-1.1	1.0	-1.1	-1.2	1.1	-1.2	1.2	-1.26277	-2.3	-1.0	-1.0	-1.0
W10293 androgen regulated vas deferens protein	1.2	1.4	-1.1	1.4	1.2	-1.3	-1.3	1.5	-2.3	1.2	-1.0	1.8
AA17045 forkhead box C2	-2.5	1.1	1.4	1.4	1.1	1.7	-1.7	-3.0	-2.3	-1.6	-2.5	-1.1
AA44845 cell division cycle 2 homolog (S. pombe)/like 2	-2.1	-1.1	-1.3	1.4	1.1	2.5	-1.5	-3.0	-2.3	-1.5	-2.4	-1.4
AA22174 regulator of G-protein signaling 2	1.0	-1.7	-1.4	-1.3	1.2	-1.28201	-1.0	-1.0	-2.3	-1.1	-1.3	-1.3
AA61862 RIKEN cDNA 0810001A18, gene	1.8	1.3	-1.1	-2.5	-14.7	-2.6	1.2	-1.3	-2.4	-1.3	-1.1	-1.3
AA82132 cytochrome c oxidase, subunit VI, a, polypeptide 2	1.1	-1.3	1.1	-1.0	1.1	-1.67228	-1.2	-1.7	-2.4	1.0	-1.0	-1.4
AA08510 defensin beta 1	1.4	-1.4	1.1	-1.0	1.2	1.33028	-1.8	-1.2	-2.5	-1.1	-1.1	-1.3
AA38646 lysozin 4	1.7	1.8	1.1	-1.8	-16.9	-2.5	1.6	-1.5	-2.6	-1.1	-1.3	-1.2
W15001 CD52 antigen	1.1	-1.7	1.2	1.1	-2.3	-1.2	-1.2	-1.2	-2.5	1.1	-1.1	-1.0
AA23602 CD52 antigen	1.1	-1.6	-1.3	1.0	-1.1	-1.9	-1.6	-1.3	-2.8	-1.1	-1.2	-1.1
AA23763 rat recombinant lipid-derived mouse homology 1	2.6	1.4	-1.3	-3.9	-11.8	-2.2	1.0	-1.4	-2.7	-1.2	-1.2	-1.2
AA477023 Nrg1, mouse, 10 day old male, aortic cDNA, RIKEN full-length, cDNA, ched library, clone 1810025A17, full insert sequence	1.9	-1.1	-1.2	-2.7	-25.5	-5.2	2.1	-1.6	-2.9	1.2	-1.1	-1.4
AA171566 tropomyosin C, fast skeletal	1.1	-1.6	1.4	-1.1	1.0	1.69359	-2.0	-1.2	-3.0	-1.3	-1.3	-1.3
AA16826 ESTs	-3.2	1.4	-1.5	1.5	1.3	1.7	-1.3	-5.8	-3.0	-1.6	-3.9	-1.4
AA67074 ankyrin 2	-1.1	-1.0	1.5	1.4	1.5	1.64852	-1.2	-1.1	-3.4	-1.3	1.2	1.2
AA712003 reelin, like alpha	1.7	-1.4	-1.1	1.3	1.1	-1.65763	1.0	-1.3	-3.7	-1.1	1.2	1.4
AA675084 elastase 2	2.3	1.4	-1.2	-2.7	-21.7	-2.2	1.7	-1.9	-4.0	-1.4	-1.2	-1.4
AA170268 fibronectin 1, perinatal	1.7	2.3	-1.2	-5.8	-16.6	-5.3	1.6	-1.9	-4.1	-1.1	-1.2	-1.1
AA21587 myoglobin	-1.0	-2.5	1.0	1.1	1.0	-1.2	-1.8	-1.7	-4.3	-2.1	-1.7	-1.7
AA621684 amylase 2, pancreatic	3.1	1.1	-1.2	-2.8	-32.0	-4.0	2.5	-1.2	-4.4	-1.1	-1.1	-1.2
AA242011 serine protease inhibitor, Kazal type 3	1.5	1.8	-1.4	1.1	2.2	-1.0	-1.8	1.2	-3.2	-1.0	1.0	2.6

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TABLE 2

BLADDER

lung	spl	panc	liver	stom	col	brain	lung	blad	kidn	pl/int	mam
Description	PL 49. BDNF	PL 28. BDNF	PL 48. BDNF	PL 18. BDNF	PL 18. BDNF	PL 18. BDNF	PL 18. BDNF	PL 18. BDNF	PL 18. BDNF	PL 18. BDNF	PL 18. BDNF
AA46753 heat shock protein 70, testis	1.9	1.1	-1.0	-1.2	-1.1	-1.3	-1.8	-1.0	1.1	-1.2	1.1
AA46855 heat shock protein 70, testis	-1.2	1.2	1.1	-1.1	-1.2	-2.0	-1.7	1.1	1.1	-1.0	-1.1
AA46783 RIKEN cDNA 2310075L1 gene	1.2	1.1	-1.1	-1.1	-1.2	-1.5	-1.5	1.1	1.1	-1.4	-1.8
YB4527 milkrin 2	1.8	1.5	-1.2	-1.4	-1.2	-1.5	2.6	1.1	1.1	-1.1	-1.4
AA46874 milkrin 2	1.8	1.5	-1.2	-1.4	-1.2	-1.5	2.6	1.1	1.1	-1.1	-1.4
AA46210 FBJ osteosarcoma oncogene	-1.0	-1.3	-1.4	-1.3	-1.1	-2.3344+	1.3	2.7	1.8	1.0	1.3
AA43358 heat shock protein 70, testis	-1.7	1.1	-1.1	-1.3	-1.1	-2.0	-1.5	1.8	1.0	-1.1	-1.0
AA52375 ESTs	1.5	1.5	-1.0	1.2	1.6	-1.5	2.4	1.2	1.2	1.4	1.5
AA46630 choline kinase	1.7	1.9	-1.0	2.4	1.8	-1.35992+	1.4	2.3	1.7	2.2855+	1.8
AA46278 DnaJ (Hsp40) homolog, subfamily 3, member 1	1.3	1.12895+	1.1	1.5	1.0	1.4009+	1.1	2.2	1.4	1.2	1.4
A154924 RIKEN cDNA 0810041E03 gene	1.8	1.8	-1.3	2.6	1.9	-1.01548+	1.1	2.2	1.4	1.2	1.4
AA46682 cytochrome rich protein 81	1.1	1.1	-1.1	-1.1	-1.1	-1.03021+	-1.0	2.1	1.5	1.0	1.2
AA112878 RIKEN cDNA C590060J3 gene	1.6	1.8	-1.0	2.4	1.2	-1.3	1.3	2.1	1.8	1.5	1.7
AA07325 ESTs	1.3	1.8	-1.4	2.5	2.0	1.2707+	1.1	1.1	1.8	1.2	1.9
AA72802 RIKEN cDNA 493419D20 gene	1.1	1.1	1.4	1.0	1.5	1.09194+	-1.26553+	1.3	1.5	1.1	-1.1
A155143 ESTs. Weakly similar to Jc2378, acyl-CoA C-acyltransferase [H sapiens]	1.2	1.1	-1.4	2.4	1.3	1.05498+	1.4	1.9	1.7	1.7	1.5
AA49843 RIKEN cDNA 180017N15 gene	1.3	1.7	-1.1	2.4	1.4	1.0687+	1.4	1.3	1.6	1.4	1.8
AA200832 nuclear receptor subfamily 4, group A, member 1	-1.0	-1.0	-1.0	-1.8	-1.3	-1.08815+	-1.8	1.2	1.3	-1.0	1.1
AA005457 RIKEN cDNA 081008923 gene	1.2	-1.1	1.3	1.1	-1.1	-1.4	-2.3	-1.9	1.1	-1.3	-1.1
A152768 ESTs. Weakly similar to NP1, MOUSE RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 1, Muscular	1.1	-1.2	-1.1	1.5	1.0	1.8964+	1.1	-1.9	1.3	1.5	-1.1
A152553 scopoliprotein E	1.2	1.3	1.8	-1.7	1.5	-1.0	1.5	-1.9	1.3	1.5	-1.1
AA76973 ATPase, H+ translocating, lysosomal (vacuolar protein pump) 45D	-1.5	1.4	1.3	1.0	1.4	1.9	-1.1	-1.9	1.3	-1.5	-1.2
A152605 cdcin-dependent kinase inhibitor 1A (P21)	-1.1	-1.1	1.2	1.3	1.0	-1.04035+	-1.6	-1.8	-1.5	-1.3	-1.0
AA103046 elongator_C1_very_long_chain_1my_2acid (PENT102_SURF103_very_long_2)	-1.4	1.2	1.3	1.1	1.3	1.5	-1.7	-1.9	1.7	-1.0	-1.7
AA05184 endoprotein A-1	1.1	1.3	-1.0	1.1	-1.0	-1.2	-1.6	-1.9	1.1	-1.0	1.3
AA76395 ribonuclease 1, pancreatic	1.7	2.3	1.1	-1.2	-1.2	-1.6	-1.6	-1.9	1.1	-1.1	-1.2
AA46691 ESTs	-1.8	1.1	1.2	1.2	1.3	1.44440+	-2.17089+	-1.9	1.1	-1.2	-1.1
A155457 retinol binding protein 2, cellular	-2.0	-2.1	-1.5	-1.5	1.5	1.5	1.3	-1.9	1.6	-1.9	-1.5
AA67504 elastase 2	2.3	1.4	-1.2	-2.7	-2.1	-2.2	-1.7	-1.9	1.0	-1.4	-1.4
AA82405 RIKEN cDNA 261026H15 gene	-1.0	-1.2	1.3	-1.5	-1.3	1.2	-1.7	-1.9	1.1	1.0	-1.4
AA107035 guanidate cyclase activator 2b (ratia)	-1.2	-1.3	1.1	-1.1	2.1	2.2	-1.5	-1.0	-1.2	1.2	-1.3

TABLE 2

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AA572940 RIKEN cDNA, 170014P02, gene	-1.0123+	-1.0036+	2.1	-1.2	1.2	1.1634+-	1.2680+	-1.9	1.3	-1.0	-1.2	-1.2
WT6265 cytochrome c oxidase, subunit VIIa-1	-1.0	-1.8	-1.0	-1.1	-1.2	-1.2	-1.1	-1.9	-1.3	-1.1	1.0	-1.8
AA110072 Pih1c domain, EST	1.0	-1.7	1.7	-1.1	1.0	2.5666+-	3.2	-1.9	1.0	1.3	-1.3	1.1
AA572823 tyrosinase, 23-kDa cytochrome	-1.0	-1.0180+	1.4	1.1	1.1	1.1083-	-1.2892+	-2.0	-1.1	1.1	-1.1	-1.1
AA259775 gap junction membrane channel protein beta 1	1.2	1.1	1.4	-1.5	-1.8	1.1	-1.6	-2.0	-1.2	1.3	-1.3	1.2
AA059404 ESTs, Moderately similar to prolactinase inhibitor NP31, subunit 1H (suplex)	-1.3	1.2	2.0	1.1	1.3	2.7	-1.7	-2.0	-1.3	-1.2	-1.5	-1.1
AA517324 ESTs, Moderately similar to CVR1(TG)-	1.01627+	-1.0773+	1.1	-1.0	-1.1	1.11102+-	1.00678+	-2.0	-1.0	-1.0	1.3	1.0
AA046845 Tyrosine, 3-monooxygenase, cytochrome P-450	-1.3	1.3	1.4	-1.1	1.2	1.5	-1.2	-2.0	-1.5	-1.2	-1.8	-1.1
AA05764 myofibrin	-1.2	-1.5	-1.5	-1.5	-1.2	-1.2	-1.1	-2.0	-1.2	-1.2	-1.3	-1.4
WB6817 zinc finger protein 37	-1.5	-1.1	1.2	-1.2	1.1	1.2	-1.4	-2.0	-1.7	-1.3	-1.8	-1.4
AA437853 RIKEN cDNA, 120013J08, gene	-1.6	1.0	1.4	1.4	1.3	2.4876+-	-1.4	-2.0	-1.7	-1.1	-2.0	-1.3
AA414078 DNA segment, Chr 1, BRAT0, Dpl 466, expressed	-1.7	1.2	1.4	1.2	1.2	2.88516+-	-1.0	-2.0	-1.4	-1.1	-2.5	-1.2
WA00304 ESTs	-1.2	1.3	2.2	1.5	1.6	1.83416+-	-1.0	-2.0	-1.4	-1.3	-2.0	1.0
AA567397 leopoldin-1, cardiac	1.4	-1.6	-1.1	-2.1	1.3	1.41287+-	-2.0	-2.0	3.22	3.58728+-	-1.0	1.3
AI050580 rust related transcription factor 3	-2.0	1.1	1.2	1.4	1.4	1.86534+-	-1.75763+	-2.0	-1.8	-1.3	-1.9	-1.0
WB6896 hemoglobin X, alpha-like, embryonic chain in Hba complex	1.1	-1.6	-1.3	-1.2	-2.2	1.11032+-	-2.1	-2.0	1.0	-1.2	-4.0	-1.8
AA471393 cytochrome P450, 2010	1.2	-1.4	1.3	-1.0	1.4	1.0	1.2	-2.0	1.2	1.1	-1.1	-2.0
AI053333 hepatic nuclear factor 4	1.0	1.1	1.4	-1.1	1.1	-1.3	-1.7	-2.0	1.3	1.2	-1.1	1.2
AI053309 RIKEN cDNA, 221041J05, gene	-1.8	-1.8	-1.4	-2.1	-1.9	1.1	-1.5	-2.0	-1.8	-2.1	-1.5	-2.1
AA475351 cytochrome P450, steroid inducible 3a19	1.1	-1.1	1.4	-1.1	1.3	1.85921+-	1.3	-2.0	1.1	1.0	1.3	1.1
WB2007 neuron specific gene family member 2	-1.5	-1.5	-1.9	-2.3	-1.3	-1.0	1.4	-2.0	-1.8	-1.4	-1.3	-1.5
AA050594 solute carrier family 27 (fatty acid transporter), member 2	-1.3	-1.5	1.4	1.4	-1.0	1.8765+-	-1.3	-2.0	-1.1	1.2	1.1	1.1
AA231099 medlin	-1.8	1.3	1.1	2.3	1.2	3.3	1.0	-2.0	1.3	-1.2	-1.7	1.0
AA010759 mini chromosome maintenance deficient 6 (S. cerevisiae)	-1.4	1.1	1.1	1.1	1.3	1.5	-2.9	-2.0	-1.4	-1.3	-1.6	-1.1
AA030960 poliovirus receptor-related 1	-1.8	1.3	1.1	1.3	-1.0	1.3	1.7643+-	-2.0	-1.5	-1.4	-1.7	-1.3
AA410701 probable stem cell antigen	-1.1	-1.4	-1.3	-2.1	-1.1	1.51614+-	-1.8	-2.1	-1.0	-1.1	-1.4	-1.4
AA474101 tumor-associated calcium signal transducer 2	-2.8	-1.1	1.5	1.3	1.2	1.3333+-	-1.7	-2.1	1.5	-1.5	-2.4	-1.2
WT3719 small EDR/tyrosinase factor 1	1.1	1.1	1.0	-1.0	-1.0	1.86959+-	1.1	-2.1	-1.1	-1.1	-1.1	-1.3
AA527485 ESTs, Weakly similar to retinal short-chain dehydrogenase/reductase mEHD1 (Mus musculus)	1.7	1.6	2.1	1.1	-1.2	2.0363+-	1.5	-2.1	1.2	-1.2	1.0	1.7
AA067009 methionine adenosyltransferase 1, alpha	1.4	1.3	1.2	1.3	1.3	1.280+-	-1.5	-2.1	1.3	1.1	1.2	1.4
WT6548 alpha internexin neuronal intermediate filament protein	1.3	-1.2	-1.2	1.4	1.0	3.5715+-	1.2	-2.1	-1.2	-1.4	-1.4	-1.6
AA683322 calpain_1	-1.2	-1.4	-1.1	-1.1	1.1	-2.6	-1.7	-2.1	-1.5	-1.2	-1.4	-1.0

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TABLE 2

LUNS

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PCT/US02/41825

AA235233	forrest1 box D3	-1.5	1.0	1.4	1.0	1.2	3.5	-1.4	-2.1	-1.5	-1.9	-1.7	-1.3
AA222366	inhibitor of DNA binding_4	-2.0	1.3	1.2	1.5	1.4	2.60844	-1.1	-2.1	-1.1	-1.5	-1.6	-1.2
AA095993	MUS_hormog_5 (IE, old)	-1.5	1.3	1.7	1.3	1.3	2.2814	-1.0	-2.1	-1.4	-1.3	-1.8	-1.0
AA095994	RKEN_GDNA_2600001817_gene	-1.5	1.1	1.3	1.4	1.1	2.4	-1.2	-2.1	-1.3	-1.2	-1.8	-1.3
AA095992	carbonic anhydrase_3	1.1	1.1	3.7	1.5	1.1	-2.4	-1.7	-2.1	-1.3	-1.2	-1.6	-1.5
AA060330	Public domain EST	-1.5	-1.0	1.5	1.2	1.2	1.8333	-1.5	-2.2	-1.1	-1.2	-2.2	-1.1
AA049050	inter-alpha-trypsin inhibitor, heavy chain_4	1.5	1.3	1.2	-1.2	-1.0	1.05302	-2.1	-2.2	1.7	1.1	1.4	1.3
AA017395	Mus_musculus_MPR59_mRNA_for_mitochondrial_ribosomal_protein_S8_pooled	-1.2	-1.1	1.3	1.3	1.3	2.8	-1.9	-2.2	-2.2	-1.0	-1.4	-1.3
AB100460	Mus_musculus_high-	-1.3	-1.4	-1.1	-1.3	-1.1	2.21737	-1.2	-2.2	-1.3	1.2	-1.4	-1.2
AA017395	ability_Na-H-transporter-like cotransporter NaDC3 mRNA, complete cds	-1.3	-1.4	-1.1	-1.3	-1.1	2.21737	-1.2	-2.2	-1.3	1.2	-1.4	-1.2
W08647	non-catalytic region of tyrosine kinase adaptor protein_2	-1.8	1.1	1.3	1.0	1.2	1.4	-2.2	-2.2	-1.8	-1.3	-1.9	-1.2
AA075670	neuronal peptide precursor type A	1.1	-1.8	1.2	1.3	-1.1	2.47657	-1.3	-2.2	-1.8	1.2	-1.4	-1.7
AA037068	cytochrome_P450_3a25	1.5	-1.2	1.3	-1.1	4.0	2.87783	-1.1	-2.2	1.2	1.1	1.0	1.3
AA074621	folate receptor_1 (adult)	-1.1	-1.3	1.2	1.3	1.1	1.5	-1.2	-2.2	-1.4	1.2	-1.2	1.3
AA075277	anti-alpha trypan inhibitor, heavy chain_1	1.2	-1.2	1.1	-1.0	1.3	1.71355	-1.86147	-2.2	1.2	-1.3	-1.0	-1.1
AA087621	S-phase kinase-associated protein_2 (p46)	-1.8	-1.2	3.0	1.5	1.2	2.4757	-1.73102	-2.2	-1.8	-1.4	-1.9	-1.1
AA066739	RKEN_GDNA_2600001817_gene	-1.6	1.3	1.5	1.0	1.3	1.2	-1.4	-2.2	-1.5	-1.3	-1.8	-1.2
W08030	Friedrich allele	-1.5	1.1	1.4	1.1	1.2	1.84415	-1.6	-2.5	-1.5	-1.4	-1.7	-1.3
AA066935	contaminated binding globulin	1.0	1.2	1.6	-1.1	1.2	1.4	-2.4	-2.5	1.1	-1.0	-1.3	-2.4
AA074450	RKEN_GDNA_130007005_gene	1.3	-1.8	3.7	1.2	1.3	3.4466	-1.2	-2.4	1.1	-1.1	-1.0	-1.1
AA061492	ESTs	-2.0	1.3	1.1	-1.2	1.1	1.1	1.0	-2.4	-1.5	-1.7	-1.1	-1.1
AA042560	cytochrome_P450_1a2, aromatic compound inducible	1.3	-1.5	1.4	-1.1	-2.6	-1.33486	-1.37353	-2.4	1.8	1.1	1.2	1.2
AA028306	complement component_4 binding protein	1.5	-1.1	1.2	-1.4	1.2	-1.42054	-1.1	-2.4	1.4	-1.3	1.1	1.0
AA042560	cytochrome_P450_1a2, aromatic compound inducible	-1.1	-2.0	-1.8	-1.0	-1.8	-2.3	-1.5	-2.4	-1.4	1.3	-1.4	-1.4
AA061492	ESTs	1.5	-1.4	1.4	-1.0	-1.0	-1.16601	-1.84335	-2.4	-1.1	-1.1	-1.1	-1.1
W08217	apolipoprotein CIV	1.4	-1.1	1.3	-1.1	1.0	-1.17664	-1.2	-2.4	1.1	1.1	1.1	1.1
AA0425413	asialoglycoprotein receptor_1	-1.6	1.2	1.2	1.5	1.5	3.3711	-2.0	-2.4	-1.4	-1.6	-2.0	-1.9
AA060819	RKEN_GDNA_1190020423_gene	-2.3	1.0	1.2	-1.0	1.2	2.4	-1.3	-2.5	-2.1	-1.4	-2.6	-1.4
AA036675	protein	-1.7	-1.4	1.1	1.6	1.2	1.2	4.6	-2.5	1.6	-1.2	-2.0	-1.5
AA075278	small muscle protein, X-linked	-1.7	-1.0	1.4	1.1	1.1	2.9703	-1.4	-2.5	-1.7	-1.5	-2.1	-1.5
AA047003	lipoproteinase (DMA) III beta	-1.2	1.4	2.1	1.7	1.6	3.6	1.1	-2.6	-1.4	-1.4	-2.3	-1.1
W05270	ESTs	-2.6	-1.1	1.0	-1.4	1.2	1.2	-1.0	-2.6	1.0	1.1	-2.2	-1.5
AA026891	ESTs	1.0	-1.1	2.8	1.1	1.8	1.5	-1.2	-2.6	1.0	1.1	-2.1	-1.5
AA081013	cytochrome_P450_2c37	-1.2	-1.8	-1.4	-1.9	-1.5	1.4	-1.5	-2.6	-1.2	-1.6	-1.2	-1.8
AA022987	insulin-like growth factor_2	1.3	-1.3	1.5	1.0	-1.1	1.91046	-1.1	-2.7	1.0	-1.6	-1.1	1.1
AA193412	UDP-glucuronosyltransferase_2 family_member_5	1.3	-1.3	1.5	1.0	-1.1	1.91046	-1.1	-2.7	1.0	-1.6	-1.1	1.1

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TABLE 2

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A0367219, mitral binding protein 4, plasma	1.1	-1.5	1.3	1.1	1.1	1.3	-1.8	-2.7	1.0	-1.2	-1.6	-1.5
VC430 serine protease inhibitor 1-4	1.3	1.3	-1.2	1.1	-1.2	-1.8	1.1	-2.7	1.0	-1.1	1.2	1.2
A048430, activin receptor interacting protein 1	-1.9	1.4	1.3	1.5	2.0144	-1.0	-2.7	-1.4	1.1	-1.9	1.3	1.3
A080366, vitronectin	1.1	1.5	1.3	1.1	-1.1	2.0376	-1.2	-2.9	-1.1	-1.3	-1.4	-1.3
A045887, oncosuoid 2	1.3	-1.4	1.5	-1.6	-1.4	-1.70095	-1.6	-3.0	-1.2	-1.4	-1.6	-1.6
A041427, tumor-suppressor, subchromosomal transferable fragment 3	-2.1	1.1	1.8	-1.2	1.1	2.27455	-1.8	-3.0	-1.1	-1.8	-2.9	-1.0
A046845, cell division cycle 2 homolog (S. pombe) like 2	-2.1	-1.1	1.3	1.4	1.1	2.1	-1.5	-3.0	-2.3	-1.5	-2.4	-1.4
A017645, forsyth box C2	-2.5	1.1	1.4	1.1	1.4	1.1	-1.7	-3.0	-2.3	-1.6	-2.8	-1.1
A019110, penin (or penin) proteinase inhibitor, chain E (chain 2, subunit 1), pigment, cytosol, derived from Bombyx mori	1.7	-1.1	1.5	-1.1	-1.1	-1.30539	-1.2	-3.1	-1.1	1.4	-1.6	-2.2
A035950, complement component factor 1	1.3	-1.2	1.7	-1.5	-1.6	-1.70095	-1.2	-3.1	1.1	-1.0	-1.6	-1.1
A071725, ESTs. Weakly similar to zell finger protein 65 [M.musculus]	-2.4	-1.2	1.3	1.2	1.2	1.3115	-2.0	-3.3	-2.2	-1.4	-2.4	-1.4
A018385, cyclochrome P450, 2d6	1.0	-1.0	1.6	-1.6	1.3	1.2	-1.3	-3.4	-1.2	1.3	-1.9	-1.7
A018382, small inducible cytokine A6	1.4	-1.5	1.4	-1.4	-1.1	1.0114	-1.3	-3.4	-1.0	1.2	1.5	1.4
A021274, murinoglobulin 2	1.1	-1.6	1.3	1.0	1.1	2.00205	-2.2	-3.6	1.0	1.0	-1.4	-1.1
A0106793, plasminogen	-2.3	1.2	2.8	1.4	1.5	2.14133	1.1	-3.7	-2.1	-1.6	-2.8	-1.3
A047350, synaptonemal complex protein 3	1.2	-1.7	1.3	-1.4	1.7	1.1	-1.9	-3.7	1.1	-1.0	1.1	1.1
A060385, cyclochrome P450, 2d6	1.3	-1.2	1.9	1.3	1.4	1.4	1.1	-3.9	-1.1	-1.2	-1.3	-1.2
A082202, cyclochrome P450, 2c40	1.5	-1.2	1.5	1.4	1.3	1.2	1.2	-3.9	1.1	-1.1	1.1	1.1
A0733450, serine protease, inhibitor-2 related sequence 1	1.6	-1.7	1.5	-1.4	-1.2	-1.3	1.2	-4.0	-1.0	1.0	-1.1	-1.2
W4912, kallikrein binding protein	1.1	-1.8	1.3	-1.5	-1.3	-1.64885	-1.8	-4.2	-1.4	-1.2	1.2	-1.5
A111779, oncosuoid 1	1.1	-1.8	1.3	-1.5	-1.3	-1.64885	-1.8	-4.2	-1.4	-1.2	1.2	-1.5
A038069, rescuatin	1.2	-1.3	1.5	-1.1	1.2	1.00609	-1.2	-4.2	1.0	1.0	1.1	-1.2
A024517, Public domain EST	-2.5	1.8	2.0	1.2	2.3	2.7	-1.0	-4.2	-1.9	-1.2	-2.3	1.1
A0381401, serpin, amino acid P-component	1.4	-1.3	-1.2	-1.4	-1.0	-1.65109	1.0	-4.3	1.0	1.1	1.0	1.3
A016783, ESTs. Moderately similar to Ect1 protein [M.musculus]	1.2	-1.0	1.2	-1.0	1.3	1.70797	-1.4	-4.5	-1.1	-1.6	-1.1	-1.3
W34346, coagulation factor XII (fibrinogen factor)	1.1	1.1	1.2	1.1	1.1	1.07469	1.1	-4.8	-1.3	-1.1	-1.2	1.2
A027351, baselin-homocysteine methyltransferase	1.3	-1.3	2.0	-1.0	1.1	1.62439	1.1	-4.7	1.3	-1.3	1.2	-1.1
A082209, group specific component	1.5	-1.4	1.0	-1.0	1.3	-1.6	-1.4	-5.1	1.2	1.2	1.1	1.1
A038299, DNA segment, Chr 1, University of California at Los Angeles 3	-1.0	-1.5	1.65571	1.3	-1.5	1.3	-1.1	-5.1	-1.4	-1.2	-1.2	-1.5
A046451, beta acid binding protein 1, liver	-1.5	-1.5	1.4	-1.2	-1.2	1.67068	-1.3	-5.1	-1.3	-1.2	-1.3	-1.2
A071394, 4-hydroxyphenylpyruvic acid dioxygenase	1.1	-1.4	1.2	1.1	1.4	1.1	-2.1	-5.2	1.3	1.2	1.1	1.5
A018066, ESTs	-3.2	1.4	1.5	1.5	1.3	-1.3	-1.3	-5.6	-3.0	-1.8	-3.9	-1.4
A037013, murinoglobulin 2	1.7	-1.1	1.2	1.4	1.3	1.1	-1.4	-5.8	-1.2	1.0	1.1	-1.2
A060385, aldoloprotein, H	1.3	-1.3	1.4	1.4	1.2	1.77465	-1.0	-7.1	1.3	1.2	1.1	1.1
A032116, transferrin	1.2	-1.1	1.5	-1.5	-1.4	1.59327	-1.3	-7.7	-1.0	1.1	-2.0	-1.8

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TABLE 2

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AA068867_RKEN_cDNA_3010002H13_gene	1.3	-1.1	1.0	-1.1	2.0	1.48549-	1.4	-7.9	-1.1	-1.1	-1.7	-1.2
W54403_ATPase_C1+ transporth beta polypeptide	1.2	-2.1	1.1	-1.0	1.2	1.3	-2.9	-7.9	1.1	-1.1	-1.1	1.2
AA075318_aurogastrolin_1	1.5	-1.5	1.1	-1.0	1.0	2.74582-	-1.8	-7.9	-1.1	-1.1	1.3	1.0
AA467336_cytochrome_P450_sterol_reductase_3a11	1.6	-1.4	1.1	1.1	2.2	8.66111-	-1.3	-8.0	-1.0	-1.1	1.2	1.1
AA4822058_apolipoprotein_A-I	1.9	-1.5	1.1	-2.4	2.4	2.4	-1.9	-9.0	-1.2	-2.1	-2.5	-1.8
AA068337_alpha2-macroglobulin	1.3	-1.4	1.0	1.1	1.2	1.52484-	1.1	-10.5	-1.1	-1.7	-1.3	-1.2
AA422209_hemoglobin	1.1	-1.2	-1.1	1.2	1.1	2.53584-	-1.6	-11.1	1.2	-1.6	-1.3	1.2
W13873_gelatinase_inhibitor_1-5	1.1	-1.7	1.2	-1.3	-1.3	-1.1	-1.5	-14.7	-1.2	-1.1	-1.4	-1.5
W57032_serine_protease_inhibitor_1-3	1.1	-1.6	1.4	-1.5	-1.5	-1.1273-	-1.3	-15.2	-1.4	-1.4	-1.5	-1.8
AA467420_major_urinary_protein_1	1.1	-1.1	-1.1	-5.0103*	-2.7	1.0	1.09942-	1.5	-16.7	-1.5	-1.6	-1.4
AA422106_EST6_Vireally_similar_to_COBA_HUMAN_COMPLEMENT_C9	2.7	-1.7	2.2	-1.0	1.1	2.60384-	-1.8	-20.2	-1.5	-1.3	-1.4	-2.7
ALPHA_CHAIN_PRECURSOR_H.sapiens	1.2	-1.9	1.2	-1.4	-1.0	1.17894-	-1.2	-21.9	-1.5	-1.5	-1.8	-1.7
AA422027_ATPase_C1+ transporth beta polypeptide	2.5	-1.7	2.0	1.1	-1.1	1.69484-	-1.3	-23.1	-1.4	-1.5	-1.3	-2.9
AL380308_serum_albumin_variant	1.1	-2.4	-26.7549*	-7.8	-1.1	1.43224-	-1.3	-71.1	-1.6	-2.2	-1.1	-1.2
AA422106_major_urinary_protein_1	1.1	-2.4	-26.7549*	-7.8	-1.1	1.43224-	-1.3	-71.1	-1.6	-2.2	-1.1	-1.2

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TABLE 2

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train	spl	panc	liv	stom	int	col	ur	lung	blad	kidn	pilot	nam
Description	PL_45_BREWER	PL_28_BREWER	PL_18_BREWER	PL_18_BREWER	PL_38_BREWER	PL_48_BREWER	PL_18_BREWER	PL_18_BREWER	PL_18_BREWER	PL_18_BREWER	PL_18_BREWER	PL_18_BREWER
AA085763 hemoglobin beta adult major chain	1.3	-1.2	1.4	-4.0	1.1	-4.2	3.8	1.1	-4.3	1.5	-1.8	-2.0
WY8306 hemoglobin beta adult major chain	1.5	-1.2	1.2	-2.3	1.3	-3.7	3.4	-1.2	-1.0	1.8	-1.7	-1.8
WY4853 kinesin-associated protein 3	-1.0	-1.0	1.4	3.2	-1.2	-3.932+	4.3	-1.2	-1.2	1.3	-1.5	-1.5
AA1410071 hemoglobin beta adult major chain	1.3	-1.4	1.2	-3.0	-1.1	-4.33	3.2	1.1	-4.3	1.8	-1.7	-2.0
AB14738 RIKEN cDNA 28130116 gene	1.3	2.0781+	1.1	2.4	1.5	1.2405+	2.8	1.4	1.5	1.8	-1.5	1.8
AA147357 ESTs	1.1	1.7	1.055+	2.9	1.883+	-1.0035+	2.9	1.6	1.7	1.8	2.1	2.1
AA14739 ESTs, Weakly similar to 23V1_MOUSE FRIEND_VIRUS 3U SCIENTIFIC PROTEIN [M.musculus]	1.2	17.1031+	-1.0739+	2.7	1.7	1.9430+	2.5	1.0739+	1.8	1.5	1.8	1.8
AA023858 protease (pase_01_batz)	-1.5	1.2	-1.8	1.3	1.1	-1.16438+	2.4	1.01988+	-1.1	-1.1	1.1	1.1
AA021854 amylase 2, cereals	3.1	1.1	-1.2	-2.8	-32.0	-4.0	2.2	-1.2	-4.4	-1.1	-1.1	-1.2
AA083876 amylase 2, cereals	1.1	1.8	-1.5	2.6	1.7	1.7791+	2.3	1.6889+	1.7	1.4	1.9	2.1
W57291, Mesh-lined, imprinted transcript, 1	1.2	1.1	1.3	1.1	-1.43302+	2.3	1.5	1.4	1.1	1.7	1.2	1.2
AA049897 RIKEN cDNA 573404015 gene	1.3	1.7	-1.0	1.1	-1.0	1.01531+	2.3	1.0	1.1	1.3	1.1	1.1
AA022944 ESTs, Moderately similar to No. simulating to amy reported protein [D. dentissima]	1.1	1.0	-1.3	2.9	-1.1	-1.30021+	2.4	1.0	-1.2	1.2	-1.2	-1.0
AA139513 ESTs, Moderately similar to P28L_MOUSE_BPF-2-KTRU-2.6-2 PHASE LIVER ISOZYME [M.musculus]	-1.2	1.1	1.1	-1.8	1.1	-2.6	2.2	1.3	-1.1	1.4	-1.3	-1.3
1.0 -1.4	1.0	1.0	1.2	-1.7	1.842+	2.1	1.2	1.1	-1.2	1.3	1.1	1.1
AA165734, acotin 3	1.1	-1.1	1.0	2.0	1.4	-1.03185+	2.1	1.09353+	1.4	1.2	1.4	1.1
AA046693 RIKEN cDNA 271001513 gene	1.3	-1.1	-1.2	-2.7	-25.5	-5.2	2.1	-1.8	-2.8	1.2	-1.1	-1.4
AA171025, Nucleoside to Jay, cat, male, pancreas cDNA, RIKEN full-length cDNA library, Gene ID1333347, full-length cDNA	-1.0	1.6	-1.0	1.7	1.0	1.2378+	2.1	1.2	1.2	-1.0	1.3	1.4
AA171555 RIKEN cDNA 118005117 gene	-1.16124+	1.5	1.37787+	1.3	1.2	-1.128359+	2.1	1.15522+	1.1	1.3	1.2	1.2
AB194945 RIKEN cDNA 633404016 gene	1.05931+	1.2095+	-1.07594+	1.2	1.0793+	-1.02044+	2.1	-1.01988+	-1.0203+	1.4	-1.1	1.078+
AA111984 liver-specific, BHLH-2b, transcription factor	1.5	1.3	-1.0	-1.0	1.5	1.3117+	-1.1	1.1	1.2	1.4	1.1	1.1
AA022311 RIKEN cDNA 810304017 gene	1.2	1.7	-1.1	1.0	1.2	-1.08779+	2.1	1.3	1.8	1.4	1.5	1.5
AA071857 brain protein	1.0	-1.0	-1.1	-1.2	-1.5	1.05332+	2.1	1.1	1.0	-1.5	1.2	1.1
AA023944 ESTs	1.4	1.3	1.0	3.7	1.1	-1.54029+	2.0	1.3	1.49495+	1.2	1.4	1.2424+
AA102518, microtubule-associated protein 6	1.1	1.0	-1.8	-1.4	1.1	1.28694+	2.0	1.1	-1.0	-1.1	-1.2	-1.1
AA104348 RIKEN cDNA 3110232501, S908	1.0	1.2	-1.4	1.8	1.5	1.0555+	2.1	1.2	-1.0	1.1	-1.0	-1.0
AA080809, Abcam/Commins, A-associated protein 2	1.4	-1.2	-1.3	2.1	1.4	-1.5	2.1	1.5	1.5	1.2	1.4	1.1

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TABLE 2

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AA0200457 ESTs	-1.4	1.2	-1.5	-1.1	1.19197*	1.00394**	-2.0	-1.2	-1.1	1.1	-1.3	-1.1
AA0234330, glycophosphatidylinositol-specific phospholipase D1	-1.1	-1.3	1.2	-3.4	2.3	-1.5	2.0	-1.2	-1.3	1.2	-1.6	-1.6
AA0290346, amyloid, epithelial, desmin-like, type II	-1.4	1.0	-1.5	-1.3	1.1	-1.06374*	3.0	-1.2	-1.0	-1.4	1.1	
AA0123314 ESTs, highly_antisense_588176, TOG protein [H.sapiens]	1.1	-1.0	-1.2	-1.0	1.1	-1.0557*	2.0	1.3	-1.1	-1.0	-1.1	-1.2
129138*	1.55183*	-1.01924*	2.3	1.37739*	-1.21581*	1.50659*	3.807*	1.62081*	2.24475*	1.7355*		
AA0173684, RIKEN cDNA, C03002077 gene	1.2	1.4	-1.4	1.0	1.5	-1.5	2.0	-1.4	-1.4	1.5	1.6	
AA0158166 ESTs	1.2	1.4	1.0	2.1	1.4	-1.20027*	1.7	1.8	-1.4	1.6	1.5	
AA0112821, RIKEN cDNA, 42741402, gene	1.4	1.6	1.0	1.0	1.1	1.17254*	1.30381*	1.5	-1.0726*	1.10775*	-1.1	-1.20281*
AA0051041, ribosomal, cytochrome c1, alpha, subunit, O, member 2	1.1591*	1.9792*	1.2	2.956*	-1.0	1.17254*	1.30381*	1.5	-1.0726*	1.10775*	-1.1	-1.20281*
AG045487 ESTs	1.2	1.3	-1.1	2.3	1.5	-1.02044**	1.5	1.5	1.3	1.5	1.6	
AA0050783 ESTs	1.14485*	-1.03044*	1.09581*	1.1	1.06555*	-1.18692*	1.3	1.15474*	1.1	1.2	1.1	-1.1
AA0050783, Public domain EST	1.0	-1.11378*	1.32861*	1.2	-2.4	-1.61477*	1.9	1.63479*	1.2	1.3	1.1	-1.83715*
AA0468153 ESTs	1.0	-1.16408*	1.12055*	-1.34277*	-1.48418*	-1.47895*	1.3	1.03133*	-1.14819*	1.0	1.0	-1.0
AA022952, zooth related factor 2	1.0	-1.0	-1.1	1.4	1.4	-1.46783*	1.1	1.1	1.1	1.2	1.2	
AA0416143 ESTs	1.08864*	-1.2	-1.0035*	1.4	1.2	-1.04533*	1.9	1.00653*	-1.1	1.0	-1.1	1.2
AA0592323, RIKEN cDNA, 150001-0303	1.26047*	1.62377*	-1.04077*	1.88417*	1.6324*	1.50262*	1.9	1.37534*	1.4	1.5	1.4	1.98519*
AA03202, ribosomal protein S6	1.2	1.5	1.0	2.2	1.2	-1.20382*	1.0	1.3	1.4	2.1	1.7	
AA0511234 ESTs	-1.1	1.1	-1.3	1.1	-1.6	-1.65331*	1.9	1.0	-1.2	-1.1	-1.1	1.0
AA050872, RA0119, member, RAS oncogene, family	-1.1	-1.3	-1.6	1.3	1.6	-1.31004**	1.3	1.3	1.2	1.2	1.2	1.4
AA0385004 ESTs	-1.8	-1.1	-1.52515*	-1.2	1.0	-1.39693**	1.0	1.0	-1.3	1.2	-1.1	-1.3
AA120302 ESTs	-1.2	1.1	-1.2	1.3	1.4	-1.30774*	1.6	1.1	-1.1	1.1	1.0	1.2
AA121912 ESTs	1.2	1.5	-1.4	2.2	1.5	-1.07075*	1.3	1.4	1.7	1.2	1.5	1.6
AA035144 ESTs	-1.50111*	-1.02049*	1.0398*	1.1	1.00924*	1.053391*	1.3	-1.02865*	1.1	1.4	1.1	1.0
AA037339 ESTs	-1.2	1.0	1.1	-1.5	-1.7	-1.14348*	-1.9	-1.1	-1.1	-1.1	-1.0	-1.1
AA0738833, solute carrier, family, 1, member, 7	1.2	-1.2	-1.5	-1.7	-1.2	1.0	-1.9	-1.2	-1.1	-1.0	1.1	-1.5
AA038395, cholesteryl-cholesterol transferase P450, 289	1.2	-1.7	1.3	-1.4	1.7	1.1	-1.9	-3.7	1.1	-1.0	1.1	1.1
V03045, autophagic translocation initiation factor 4E, b2/alpha protein, 1	1.0	1.3	1.1	-1.2	1.0	-1.0	-1.9	-1.2	1.0	-1.0	-1.1	-1.2
V03570, deslin	-1.2	-1.4	-1.3	-1.7	-1.2	1.1	-1.9	-1.0	-1.1	1.3	1.9	-1.3
AA07113, myosin heavy chain, cardiac, muscle, adult	-1.0	-1.3	-1.1	1.7	2.0	2.2	-1.9	1.3	1.2	-1.0	1.5	1.3
AA0585219, Integrin	-1.9	-1.5	1.1	-2.4	2.4	2.4	-1.9	-6.0	-1.2	-2.1	-2.5	-1.6
AA022008, apolipoprotein A-I	-1.1	1.0	1.2	1.0	-1.0	1.1	-1.9	-1.1	1.1	1.1	-1.1	1.1
AA02604, cyclin F	-1.1	1.0										

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A475268, solute carrier family 4 (anion exchanger), member 1	1.0	-1.5	1.1	-1.1	1.2	-1.5	-1.1	-1.2	-1.5	-1.1	-1.2	-1.5	-1.1
A475317, solute, transmembrane transporter 1 (soluble)	1.0	-1.1	1.3	1.1	-1.1	-1.6	-1.2	1.1	-1.2	1.0	-1.1	-1.6	-1.1
A484001, ESTs	-1.00433+	-1.00455+	1.02444+	1.02571+	-1.14302+	-1.23033+	-1.3	-1.2	-1.1	-1.28311+	-1.0	-1.07084+	1.00265+
A484015, public domain EST	1.2	-1.3	1.2	1.5	1.2	2.23333+	-1.0	-1.2	1.3	2.0	1.0	1.4	1.4
W0245, ESTs	-1.2	1.4	-1.1	-1.4	-1.3	1.3	-1.5	-1.5	-1.2	-1.3	-1.2	1.0	1.0
A481578, RIKEN cDNA, 1600013P15, gene	-1.3	-1.4	1.3	1.0	-1.8	1.722+	-1.5	-1.1	-1.0	-1.2	1.0	1.0	1.0
A486245, immunoglobulin, light chain	1.2	-1.5	-1.4	-1.2	-2.2	-2.4	-1.8	-1.1	1.3	1.5	1.4	-1.3	1.5
A487138, proteinase A2, group IIA (platelet, granular, fluid)	-1.1	-1.0	-1.2	1.3	2.1	1.4	-1.8	-1.3	1.5	1.2	1.3	1.5	1.5
A487142, cathepsin (N-acetylglucosaminase, C-1, sulfatransferase 5)	1.0	1.4	-1.1	1.3	1.2	1.07754+	-1.1	1.2	-1.1	1.0	1.0	1.1	1.1
A477943, ESTs, weakly similar to A53359 L8 antigen - mouse [M.musculus]	-1.2	-1.1	1.4	-1.1	-1.3	0.8125+	-1.6	-1.1	1.1	1.2	1.1	1.1	1.7
A485795, glycin-rich protein 2	1.2	1.1	1.5	-1.6	-1.3	-1.3	-1.8	-1.5	-1.2	-1.1	-1.2	-1.3	-1.3
A444413, immunoglobulin heavy chain 6 (heavy chain of IgM)	-1.2	-1.8	-1.4	1.1	1.2	-2.1	-1.9	-1.1	1.0	-1.0	1.2	1.0	1.0
A485522, RIKEN cDNA, T000226C01, gene	-1.2	-1.4	-1.0	-1.1	-1.3	1.2	-1.9	-1.2	-1.1	-1.1	-1.1	-1.1	-1.1
A485407, tropomyosin, T1, skeletal, slow	1.1	-1.2	1.3	-1.1	1.2	1.5445+	-1.5	-1.1	-1.0	1.1	1.1	-1.5	1.5
W18463, pleckstrin, Smad3/transferrin	1.0	-1.5	2.0	-1.3	-1.6	-1.6	-1.6	-1.0	-1.7	1.2	-1.0	-1.2	-1.0
A485552, Mus musculus, class IIAC25-3449758, cDNA, partial cds	-1.0	-1.2	1.2	1.1	1.1	1.3302+	-1.3	-1.2	1.0	-1.2	1.0	-1.0	-1.0
A487155, Mus musculus, M19584, RNA for ribonucleic acid-associated protein, S8, partial cds	-1.2	-1.1	1.3	1.3	1.3	2.1	-1.9	-2.2	-1.2	-1.0	-1.4	-1.3	-1.3
A414564, ESTs	-1.2	-1.4	-1.4	-1.5	-1.1	-1.0344+	-1.9	-1.1	-1.3	-1.2	-1.1	1.3	1.3
A4022420, small protein-rich protein 1A	1.3	-1.7	-1.4	-1.5	-1.9	-1.2	-1.9	-1.2	1.0	-1.1	1.3	1.3	1.3
A417437, RIKEN cDNA, T700291P1, gene	1.0	-1.2	1.2	1.0	1.2	1.40773+	-1.8	-1.2	-1.1	-1.1	-1.2	-1.3	-1.3
A4103767, soluble center family 22 (organic cation transporter) 2	-1.2	-1.0	-1.1	-1.3	-1.3	1.2	-1.9	-1.0	-1.1	1.2	-1.1	-1.1	-1.1
A402513, RIKEN cDNA, Z910401C01, gene	1.1	-1.2	1.1	-1.2	-1.7	1.4	-1.9	-1.0	-1.1	1.0	1.1	1.0	1.1
A4871284, tropomyosin, T2, cardiac	1.0	-1.7	-1.3	-1.1	-1.2	-1.0	-1.9	-1.6	1.1	1.4	-1.2	-1.2	-1.2
A484812, ESTs, weakly similar to A51833, leucosarcosine-resistant, immunoglobulin-associated protein, PF38 - mouse [M.musculus]	-1.2	-1.2	1.1	-1.1	1.3	1.4625+	-1.6	-1.1	-1.2	-1.4	-1.1	-1.4	-1.4
A418190, cyclohexane, P40, subfamily IV B, polypeptide 1	1.0	-1.4	-1.1	-1.1	1.1	1.6	-1.9	-1.2	-1.2	1.1	-1.1	-1.1	-1.1
A478452, Mus musculus, class IIAC25-3449758, cDNA, complete cds	1.3	-1.4	-1.3	-1.5	-1.4	-1.3023+	-1.9	-1.2	-1.1	-1.1	-1.1	1.1	1.1
A411702, cytosolic, granule-associated RNA-binding protein 1	1.3	-1.1	1.1	-1.0	1.1	-1.1	-1.9	1.0	-1.0	-1.2	1.0	-1.0	-1.0
A454749, myosin Ic	-1.1	-1.1	1.0	-1.2	-1.4	1.0	-1.9	1.1	-1.1	-1.0	-1.1	-1.1	-1.2
A475268, N-myc, lard, STAT1, inhibitor	1.3	-1.5	1.0	-1.2	-1.9	-3.2	-1.9	-1.0	-1.2	-1.0	-1.1	-1.4	-1.4
A475268, immunoglobulin, heavy chain 6 (heavy chain of IgM)	1.0	1.1	-1.0	-1.2	-1.0	-1.5	-1.1	-1.1	-1.0	-1.1	-1.0	1.1	1.1
W03337, ribonuclease, activated, protein kinase 13	-1.1	-1.2	1.1	-1.1	-1.2	1.24334+	-2.0	-1.1	-1.1	-1.1	-1.3	1.0	1.0
A4850430, myeloblastosis oncogene-like 2	-1.2	-1.2	1.5	1.0	-1.2	1.0218+	-2.0	-1.2	1.1	-1.3	-1.0	1.2	1.2
A485280, N-myc, lard, STAT1, inhibitor	-1.0	-1.5	-1.3	1.1	1.2	1.0218+	-2.0	-1.1	-1.2	-1.2	-1.0	-1.0	-1.0
A475268, immunoglobulin, heavy chain 6 (heavy chain of IgM)	1.0	-1.5	-1.3	1.1	1.2	1.0218+	-2.0	-1.1	-1.2	-1.2	-1.0	-1.0	-1.0
A485280, N-myc, lard, STAT1, inhibitor	1.4	-1.3	-1.4	1.5	1.2	1.05991+	-2.0	1.3	1.2	-1.1	1.5	1.5	1.5

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TABLE 2

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AA080616_RIKEN_CDNA_150001293_gene	-1.6	1.2	1.2	1.5	1.5	3.3219e-20	-2.0	-2.4	-1.4	-1.6	-2.0	-1.3
AA081930_phospholipase_A2_group_IIIC	-1.3	1.0511e-1	1.3	1.1	1.1	1.6331e-4	-2.0	-1.2	1.1	1.0	-1.2	1.3
AA021893_keratocornea.1	1.0	-1.6	1.6	1.0	1.3	1.3038e-1	-2.1	-1.4	-1.1	-1.2	-1.0	-1.1
AA115441_gene_dcl_cluster_C8_gene	1.1	-1.3	1.3	1.2	1.1	1.4	-2.1	-1.3	1.1	1.3	-1.1	1.0
W0995_hemoglobin_X_alpha-like_erythrocyte_chain_in_Hba_complex	1.1	-1.6	-1.3	-1.2	-2.2	1.1120e-2	-2.1	-2.0	1.0	-1.2	-4.0	-1.6
AA171395_4-hydroxyphenylpyruvate_dioxygenase	1.1	-1.4	1.2	1.1	1.4	1.1	-2.1	-6.2	1.3	-1.2	1.1	1.5
AA176023_apical_membrane_protein_3	-1.1	-1.1	1.4	-1.0	1.2	1.0434e-1	-2.1	-1.3	-1.1	-1.3	-1.2	-1.4
W05649_vacuolator-eliminated_chaperonin	1.0	-1.1	1.1	-1.3	1.1	1.1	-2.1	-1.3	-1.2	-1.2	-1.2	-1.3
AA191058_protoglycan_1_receptor_(P)	1.0106e-1	-1.10471e-1	1.00277e-1	-1.3	-1.31076e-1	-1.04094e-1	-2.1	-1.11103e-1	1.5	-1.1	1.2300e-1	1.11434e-1
AA047177_cytochrome_P450_2m4	1.2	-1.6	2.6	1.1	1.3	1.7253e-1	-2.1	1.2	-1.0	2.1	-1.1	-1.2
AA437572_lmr_centrinome_protein	1.1	-1.4	1.1	-1.3	-1.2	1.2932e-2	-2.1	-1.1	1.2	1.1	-1.0	1.1
AA102630_secretory_leukocyte_protease_inhibitor	1.1	-1.5	1.1	-1.1	1.0	1.1	-2.1	1.1	-1.0	-1.1	-1.1	-1.4
W083701_DNA_segment_Ch12_Bigham_8_Women's_Genetics_1423_poreosse	-1.2	-1.0	-1.5	-1.5	1.0	-1.6225e-1	-2.1	-1.2	-1.3	-1.2	1.1	1.0
AA194828_h1_1gand	1.0	1.10758e-1	1.00332e-1	-1.2891e-1	-1.6301e-1	-1.0631e-1	-2.1	1.1	1.1	-1.1	1.3	-1.1
AA151780_protease_specific_est_transcription_factor	-1.1	1.4	1.1	-1.5	-1.1	-2.4747e-2	-2.1	-1.0	-1.1	1.0	1.0	1.0
W11251_Fc_receptor_1e6_high_affinity_L_germna_polypeptide	1.2	1.3	1.3	1.1	1.0	1.02631e-1	-2.1	1.1	1.1	-1.1	-1.1	-1.1
AA081385_Mus_musculus_DNA_cytosine_methyltransferase_mRNA	-1.4	-1.3	1.2	1.0	1.0	1.6103e-1	-2.1	-1.6	-1.2	-1.1	-1.4	-1.0751e-1
AA324400_transforming_growth_factor_beta_receptor_II	-1.1	-1.1	1.5	1.0	1.6	1.3	-2.1	1.1	1.3	1.1	1.0	1.0
AA1733419_syndecan.1	1.1	1.1	1.1	-1.2	1.1	1.4	-2.1	1.1	-1.1	-1.0	-1.2	1.1
AA171719_TEA_domain_family_member_2	-1.3	1.1	-1.1	-1.1	-1.2	1.8281e-1	-2.1	-1.5	-1.3	-1.3	-1.1	-1.1
AA046980_ntr_alpha-tyrosin_inhibitor_baby_chao_4	1.5	1.3	1.2	-1.2	-1.0	1.0530e-2	-2.1	-2.2	1.1	1.4	1.3	1.3
AA176959_brocollagen_type_XVII_alpha.1	1.1	-1.2	1.5	-1.2	1.4	1.0433e-1	-2.1	-1.2	1.2	-1.1	1.0	-1.2
AA102678_insulin_complex_2_basic_gene_4	1.2	-1.9	-1.3	-1.0	-1.0	1.44871e-1	-2.1	1.6	1.4	-1.1	1.5	1.3
AA175591_insulin-like_growth_factor_2_receptor	-1.1	-1.1	-1.2	-1.1	-1.1	1.4	-2.1	-1.1	-1.3	-1.1	-1.1	-1.1
AA1727051_myeloid_leukemia_factor.1	1.1	-1.8	1.2	1.1	1.3	1.6554e-1	-2.1	-1.1	-1.1	-1.3	1.1	-1.4
AA173487_glycosylation_dependent_cell_adhesion_molecule.1	-1.0	-1.2	1.2	1.2	1.1	1.1	-2.1	-1.3	-1.0	-1.1	1.2	1.3
AA1444530_selenoproteinase_7 (lepho-N-acetylneuraminy_2,3-sia-galactosyl-1,3)	1.4	-1.2	-1.0	1.0	-1.2	1.2	-2.2	-1.1	-1.1	-1.3	1.2	1.5
AA046891_thymidine_kinase.1	1.2	-1.2	1.6	-1.2	-1.1	1.24771e-1	-2.2	-1.1	1.3	1.0	-1.1	1.1
AA106072_Pdlin_Jordan_EST	1.0	-1.7	1.7	-1.1	1.0	1.2363e-1	-2.2	-1.9	1.0	1.3	-1.3	1.1
AA144110_FSTs	-1.2	-1.5	-1.3	-1.2	1.0	1.0293e-1	-2.2	-1.0	-1.0	-1.1	1.1	1.1
AA141412_ethacrynicacid_inositol_glycan_class_A	1.1	-1.6	1.1	-1.1	-1.6	1.16321e-1	-2.2	1.0	-1.0	-1.0	1.2	1.2
AA104582_actin_dihydroxyphenylglyoxanase_3_C_chain_isom_glycolic	1.2	-1.6	-1.3	1.5	1.3	1.2782e-2	-2.2	-1.0	-1.1	1.0	1.7	2.4
AA170958_RIKEN_CDNA_270001H007_gene	-1.2	1.2	1.2	-1.4	-1.5	1.0	-2.2	-1.2	-1.2	-1.3	-1.1	1.0
W16012_dengbion	1.3	-1.6	1.2	-1.4	-1.6	1.0	-2.2	-1.3	-1.2	1.1	-1.2	-1.3

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TABLe 2

BRAIN

TABLE 2

A4A102940	immunoglobulin kappa chain variable 2B (V2B)	1-3	-1.6	-1.5	-1.0	-2.1	-3.1	-2.2	-1.3	-1.3	0.6	-1.1	-2.5
A3A28527	perlecanin	-1-3	-1.2	-1.0	-1.2	1.0	-1.5975	-2.2	-1.3	-1.1	-1.2	-1.1	1.2
A4A37628	milkogen activated protein kinase kinase theta 2	1	1.19438	1.08191*	1.10054*	-1.00411*	-1.21849**	-2.2	-1.2	-1.00084*	1.1	1.1	-1.1
A4A07483	arcelaphan secretory granule	1-2	-1.4	1.1	1.3	1.2	1.1	-2.2	-1.2	1.1	-1.2	-1.1	1.4
A4A62227	glutathione S-transferase, alpha 3	1-3	-1.0	-1.4	-1.3	-1.0	2.2	-2.2	-1.2	1.8	1.3	-1.2	1.0
A4A20024	tyrosine-specific protein	1-5	-2.0	-1.2	1.5	1.1	-1.0	-2.2	-1.2	1.1	1.2	2.3	
A4A10679	pantothien	1	-1.6	1.3	1.0	1.1	2.0235	-2.2	-3.6	1.0	-1.4	-1.1	
W03047	non-catalytic region of gamma kinase adaptor protein 2	-1.8	1.1	1.3	1.0	1.2	1.4	-2.2	-2.2	-1.8	-1.3	-1.9	-1.2
A4A03073	RIKEN cDNA 4821542F20 gene	-1.1	-1.2	-1.3	-1.4	-1.4942*	-1.22089**	-2.2	-1.2	-1.7	-1.1	-1.2	-1.2
A4A12413	chitinase-defect	-1.1	-1.3	1.8	-1.2	1.2	0.00734**	-2.2	-1.2	2.6	1.2	-1.2	-1.0
A4A27450	phospholipase A2 group IB precursor	1-3	1.8	1.1	-1.8	-5.7	1.60324*	-2.3	-1.5	-1.4	-1.4	-1.0	
A4A11754	growth arrest specific 2	-1	-1.4	1.4	1.1	1.3	1.9018*	-2.3	-1.3	1.0	-1.3	-1.4	-1.4
A4A29624	fatty acid binding protein 2 (hepatic)	-1-5	-1.5	-1.7	-1.7	-1.1	2.6	-2.3	-1.0	1.4	1.1	1.7	-2.1
W03635	carnitine modulator 2	-1-2	-1.9	-1.4	1.4	1.0	1.3	-2.3	-1.1	1.0	1.2	1.5	1.1
A4A15417	poliovirus sensitivity	-1-2	1.0	1.8	-1.1	1.2	1.3	-2.3	-1.4	-1.3	-1.1	-1.3	-1.1
A4A27037	pyruvate kinase liver and mid blood cell	-1-4	-1.2	1.8	-1.2	1.5	1.3	-2.3	-1.2	1.2	-1.1	1.0	1.1
A4A006553	claudin 7	-1	1.1	-1.2	-1.1	1.2	-1.3	-2.3	-1.2	-1.1	1.0	-1.3	-1.0
A4A18575	secreted fibzard-related sequence protein 4	1-2	-1.3	-1.4	-1.2	-1.2	1.3018*	-2.3	-1.3	1.0	-1.2	-1.3	
W15281	RIKEN cDNA 23100121S gene	-1	1.1	-1.1	1.1	1.1	-1.1	-2.3	-1.1	1.0	1.1	1.1	1.2
A4A28346	kernin complex 1, acidic, gene 19	-1-4	-1.6	-1.9	-1.5	1.0	-1.2	-2.3	-1.1	-1.1	-1.3	-1.2	-1.2
A4A1047	ascribed tyrosine-related sequence protein 2	-1-3	-1.2	-1.3	1.1	1.1	-1.0885**	-2.3	-1.3	-1.1	-1.0	1.1	-1.5
A4A02582	cytochrome P450_2I2	1-4	-1.6	1.7	-1.0	1.1	1.1	-2.3	-1.5	-1.2	-1.1	1.2	-1.0
A4A10445	dioxynucleotide 1	-1	-1.8	-1.1	-1.2	1.4	2.1	-2.3	-1.2	1.7	2.4	1.3	1.8
A4A155521	neurite-salient aminoglycine-rich	-1-1	-1.4	-1.1	-1.0	-1.1	1.5	-2.3	-1.1	-1.1	-1.3	-1.3	-1.1
A4A15949	carcin germin	1	-1.7	-1.5	1.2	1.3	1.7	-2.3	-1.3	1.0	-1.1	1.8	-1.2
A4A2575	glucose-6-phosphatase, catalytic	1-3	-1.6	1.4	1.9	1.4	1.97035*	-2.3	-1.2	1.5	1.1	1.2	1.5
A4A162782	zincfinger 5	1-3	-1.1	-1.0	-1.6	-1.8	1.63979*	-2.3	-1.1	1.0	1.2	-1.8	1.4
A4A062457	RIKEN cDNA 0610006F02 gene	1-2	-1.1	1.3	1.1	1.1	1.1	-2.3	-1.9	1.1	-1.1	1.3	-1.1
A4A263306	ESTs	-1.18303*	-1.52332*	-1.23324*	-1.2	-1.3	-1.22277*	-2.4	-1.1	1.1	1.09812*	1.1	1.5
A4A6940	hiboxo acetyltransferase	-1	-1.2	-1.3	-1.8	-1.1	-1.0371**	-2.4	-1.2	-1.0	-1.1	-1.1	-1.2
A4A56712	myosin, heavy 20/HPRP156, L skeletal muscle, adult	-1	-1.6	1	1.2	1.2	2.2	-2.4	-1.4	-1.3	1.1	-1.2	-1.3
A4A26669	deleted in zoonosisemia-like	1	-1.2	-1.1	1.0	-1.1	-1.0547**	-2.4	-1.2	-1.1	-	-	-
A4A108125	cytochrome P450_2A4	1-3	-1.3	1.3	1.4	1.4	1.0	-2.4	-1.3	1.1	2.3	1.1	1.1
A4A61484	Public domain EST	1.0	-1.5	-1.1	1.8	1.3	2.0235	-2.4	-1.2	1.3	1.0	1.4	1.8
A4A56535	cardiolipin-binding albumin	1.0	-1.2	1.6	1.1	1.2	1.4	-2.4	-2.3	1.1	1.0	-1.3	-2.4



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AA016167, Public domain, EST	-12	-14	-12	-11	-11	-24	-16	-12	-11	-11	-12
AA87895, Intracellular-associated, alpha	-11	-16	-12	-16	-11	-21	-24	-12	-13	-12	-12
AA81502, actin-3, beta muscle	-11	-17	-10	-14	13	-45	-25	-13	-11	12	-14
W17965, enzyme-specific, proline-rich, acidic protein	-14	-17	-12	-14	-12	14114	-25	-10	-13	-13	-15
AA02034, ESTs	-18	13	14	13	13	15409	-25	-14974	-16	-10	-16
AA84138, lectin, galactose binding, soluble 7	-11	-12	13	-10	12	16	-25	-15	11	10	-10
AA52711, creatine kinase, muscle	-11	-12	11	12	13	11	-25	-12	-14	-10	-11
AA83549, glutathione peroxidase 2, pseudogene 1	-13	-10	12	-19	11	24	-23	-15	11	-11	-15
AA76574, cathepsin B, protein 3	-11	-17	10	11	13	2140	-23	-16	-12	10	-11
AA82348, collagen-binding protein, la	-12	-16	-12	-10	-12	172207	-26	-16	-18	-14	-12
AA278747, ESTs	-14874	107209	111818	10	-15	-10511	-28	11	10	12	11
AA30309, gap junction membrane channel, protein alpha 4	-11	11	11	-11	11	-13782	-28	11	-11	-12	-10
AA65194, immunoglobulin kappa chain, variable 2D (V2D) (mb)	14	-12	-14	-11	-19	-28	-28	-16	-10	14	-10
W6247, albumin-like 1	13	-18	-10	11	-10	-11	-27	-15	-13	13	-12
AA02034, ESTs, moderately similar to AF03474, rat p21 <sup>ras</sup> oncogene	11	11	12	11	12	117821	-27	11	-12	-12	-11
AA19387, ESTs	11	10378	103188	10	-12	138219	-27	11	-12	-12	-11
AA84296, tumor necrosis factor receptor superfamily, member 9	13	-23	-11	-13	-13	12	-27	-13	-11	-12	11
AA832639, RIKEN cDNA, AK0011801, gene	-11	-10	14	-11	10	13759	-27	10	10	-10	-11
AA154076, transcription factor AP-2, alpha	-15	-11	-11	-14	12	13057	-27	-14	-12	-12	-11
AA12781, histocompatibility 2, Q region, locus 7	13	-14	13	-30	18	1	-28	-12	-13	-10	-13
AA75979, le-associated invariant chain	-10	-18	-16	-19	-15	-37	-23	-10	-19	-10	-13
AA81756, prothymosin, 2-cooperative 3-deoxyribose 1	12	-12	-10	-11	-11	-13	-28	-10	-10	11	-10
AA83811, histocompatibility 2, D region, locus 1	14	-12	12	-15	15	-15	-28	11	-10	-10	-11
AA27374, RIKEN cDNA, B10008K29, gene	-10	-10	-13	14	11	100792	-28	10	-12	-11	11
AA13893, ESTs, weakly similar to KIA0081, protein [H sapiens]	-12	-11	11	-14	-12	10009	-28	-10	-10	-12	-11
W1170, small inducible G-protein G12a, (leucine)	-12	-10	11	10	13	-27	-28	-11	-11	-11	-13
AA177019, ATPase, Ca++-transporting, cardiac muscle, fast twitch 1	-12	-21	-11	-15	-13	12	-28	-14	-18	-12	-11
AA018789, mitr chromosome maintenance deficient 8 (S. cerevisiae)	14	11	11	11	13	16	-29	-20	-14	-13	-16
W54039, ATPase, Cu++-transporting, beta polypeptide	-12	-21	11	-10	12	13	-29	-20	11	-11	-11
AA145479, ESTs	-12	-13	-13	-12	-10	119703	-29	-12	-13	-12	-13
AA03049, sarcoplasmic beta (cDNA, cytoplasm-associated glycoprotein)	1034	-10	-12	-14	10	149544	-29	11	-13	-14	-10
AA26235, gap junction, membrane channel protein beta 4	11	-13	11	-10	11	14931	-30	-15	-13	-11	-10
AA76519, myosin light chain, phosphotatible, cardiac, ventricle	-11	-19	-12	-14	-13	15351	-30	-18	-13	11	10
AA83807, ESTs, weakly similar to S1-PC, ubiquitin protein, gene [H sapiens]	13	-14878	10969	-15385	-11182	-16245	-30	11181	-12	11	12

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BRANN

TABLE 2

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AA212144, forkhead, box, A2	-1.2	1.7	1.2	-1.2	-1.7	1.9246+	-3.1	-1.3	1.1	-1.4	-1.5	-1.1
AA97195, Public domain EST	1.3	-1.4	-2.0	1.4	-1.7	-3.0	-3.1	-1.3	1.2	1.3	1.4	-1.7
AA27090, nuclear_receptor_subfamily_1_group_H_member_4	1.2344+	1.21202+	1.5	1.0	1.2048+	-1.3218+	-3.1	-1.0981+	-1.0072+	1.1	1.1	1.2818+
AA736972, Mus musculus mRNA for thymosin, complete cds	-1.1	-1.2	1.2	1.1	1.2	-2.725+	-3.1	-1.3	-1.2	-1.1	-1.3	-1.5
W8421, Myeloid leukemia, virus 10	-1.1	1.0	1.1	1.2	1.0	-1.6915+	-3.3	1.1	1.1	-1.1	-1.1	-1.1
AI55101, ESTs	-1.1386+	-1.0009+	-1.0009+	-1.0	1.0911+	1.2429+	-3.4	-1.1513+	-1.3	-1.3	-1.1	-1.2
AA008303, phosphodiesterase, 8D, cGMP-specific, rat, delta	1.2	-1.0398+	1.5	1.0	1.1	-1.1258+	3.4	1.0	1.1	-1.1	1.0	-1.2
AI55561, Mus musculus Rep-9 mRNA for reproduction 9, complete cds	-1.0	1.1	1.7	-1.0	-1.3	-1.1769+	-3.4	-1.1	1.0	-1.1	1.1	-1.0
AA547602, ESTs	1.1	1.2204+	1.2	1.2	-1.0	1.6789+	-3.0	-1.3	-1.0	-1.3	-1.2	-1.4
W19330, topoisomerase 2, beta	1.2	-1.3	1.0	-2.0	1.2	-1.1	-3.5	-1.5	1.1	-1.1	-1.3	-1.4
AA415771, RIKEN cDNA 111007F23, gene	1.0	-1.1	1.2	-1.3	1.2	1.1	-3.5	1.0	1.0	1.1	-1.2	-1.5
W18172, desmin	-1.0	-1.4	-1.3	-1.3	1.1	-1.8	-3.8	-1.7	-1.1	-1.1	-1.3	-1.0
AI583515, ESTs	1.0	-1.1218+	-1.6667+	-1.4	-1.2156+	-1.2621+	-3.7	1.0339+	-1.2	-1.1	1.1	1.1819+
AA154902, RIKEN cDNA 443342P12, gene	-1.1812+	1.22012+	-1.0004+	-1.1920+	-1.1371+	1.0262+	-3.7	-1.0234+	-1.0	-1.0	1.1	1.0586+
AA111724, RIKEN cDNA 533A7506, gene	-1.5	1.3	-1.4	-1.2784+	1.3	-1.6	-3.7	-1.2	-1.4	-1.1	-1.18457	-1.1
AA09186, uromodulin	-1.2	-2.0	-1.0	1.1	-1.3	1.0	-4.0	-1.4	-1.7	1.1	-1.2	-1.4
AA35138, CD8 antigen, alpha chain	-1.3	-1.0973+	-1.3	-1.8	1.2	-2.63467+	-4.0	1.0	-2.0	1.1	1.0	-1.1
AA783276, small muscle protein, X-linked	-1.7	-1.4	1.1	1.6	1.2	1.8	-4.8	-2.6	-1.6	-1.2	-2.0	-1.5
AA474017, ESTs	-1.2	-1.6	-1.1	-1.1	-1.8	1.1	-6.0	1.0	-1.2	-1.3	-1.0	-1.2

BRAIN

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TABLE 2

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colon	spl	panc	liv	stom	int	col	br	lung	blad	kidn	pituit	mam
Description	PL- 100_BDNF	PL- 100_BDNF	PL- 100_BDNF	PL- 100_BDNF	PL- 100_BDNF	PL- 100_BDNF	PL- 100_BDNF	PL- 100_BDNF	PL- 100_BDNF	PL- 100_BDNF	PL- 100_BDNF	PL- 100_BDNF
AAG56584 cytochrome P450, 21B, phenobarbital-inducible, type 2	-1.1	-1.4	1.9	1.3	2.6	3.8	-1.3	1.1	1.3	1.2	1.1	1.2
AAC31099 andrin	-1.8	1.3	1.1	2.6	1.7	3.6	1.0	-2.0	-1.3	-1.2	-1.7	1.0
AAG56592 Mus musculus Cyp11b mRNA, for family 1 cytochrome P450, complete cds	-0.0	-1.6	1.4	-1.1	1.7	3.5	-1.2	-1.1	1.0	1.0	1.2	1.1
AAG56510 RIKEN cDNA 251002C21 gene	1.1	-1.1	1.0	-1.8	1.1	3.0	-1.1	-1.0	1.4	-1.2	-1.0	-1.1
AA107035 glutathione cyclase activator 2b (retina)	-1.2	-1.3	1.1	-1.1	3.1	3.2	-1.5	-1.9	-1.2	1.2	-1.3	1.6
A225903 forkhead box D3	-1.5	1.0	1.4	1.0	1.2	3.0	-1.4	-2.1	-1.5	-1.3	-1.7	-1.3
AAG17149 Mus musculus MRP5a mRNA, for mitochondrial ribosome L16S, complete cds	-1.2	-1.1	1.3	1.3	1.3	2.9	-1.9	-2.2	-1.2	-1.0	-1.4	-1.3
AAG22473 DNA segment, Chr 5, Brilpain's, Women's, Geneset 2, 10 expressed	-1.0	-1.6	1.3	-1.0	-1.1	2.6	-1.7	-1.7	-1.2	1.2	-1.2	-1.3
AA082406 ESTa, moderately similar to, progesterone-induced hsp 70 subunit, Thapsigargin	-1.3	1.2	1.6	1.1	1.3	2.7	-1.7	-2.0	-1.3	-1.2	-1.5	-1.1
AAG17346 Rhes, muscularis, Similar to, ectonucleotide pyrophosphatase ectonucleotidase 2, clone 19A5S146525, mRNA, partial cds	1.1	-1.0	1.3	1.1	-1.3	2.6	-1.92974	-1.3	1.0	-1.1	1.0	1.2
AA518317 slug, chicken, homolog	-1.6	-1.0	1.1	1.2	1.1	2.6	-1.0	-1.8	-1.4	-1.2	-1.8	-1.3
AAG19793 methylglutathione hydrolase, dehydrogenase (NAD+ dependent), mediantoxenhydrolase, cyclohydrolase	-1.1	1.2	1.4	1.1	1.1	2.6	-1.8	-1.7	-1.3	1.1	-1.3	-1.1
AAG56524 fatty acid binding protein 2, intestinal	-1.5	-1.5	-1.7	1.7	-1.1	2.6	-2.3	1.0	1.4	1.1	1.7	2.1
AAG56521 RIKEN cDNA 2370003F10 clone	-1.4	-1.1	-1.8	-1.5	1.2	2.6	1.2	-1.6	-1.3	-1.5	-1.2	-1.1
AAG56517 RIKEN cDNA related cysteine 6	-1.2	1.1	-1.2	1.6	1.7	2.6	-1.3	1.5	1.1	1.0	1.4	1.5
AAG52172 chorista, related cysteine 6	-1.0	1.1	-1.1	1.1	1.9	2.5	-1.2	-1.2	-1.1	-1.2	-1.2	-1.5
AAG53444 forkhead box G1	-1.7	-1.0	1.7	1.5	1.5	2.6	1.1	-1.7	-1.5	-1.1	-1.6	-1.1
AAG13553 ESTa, Vastly similar to, TAD27 hypophosphatase, D5, Catecholamine release (Catechol)	-1.0	1.2	1.4	1.3	-1.0	2.6	-1.5	-1.4	-1.3	-1.2	-1.5	-1.0
AAG54674 RIKEN cDNA	2.3	1.0	1.2	-1.0	1.2	2.5	-1.3	-2.5	-2.1	-1.4	-2.6	-1.4

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TABLE 2

COLON

AA727523	IKK1, inhibitor of kappaB kinase 1	1.1	-2.0	-1.4	1.5	-1.6	1.2	1.1	1.1	1.5	1.2
AA727524	IKK2, inhibitor of kappaB kinase 2	-1.9	-1.5	1.1	-2.4	-2.4	-1.9	-8.0	-1.2	-2.1	-2.6
AA822056	POU1F1, paired box 1	-1.8	-1.7	-1.5	1.5	1.5	-1.4	-1.2	1.1	-1.2	1.4
AA85181	defensin, related, cryptidin, 6	-2.1	-1.1	1.3	1.4	1.1	-1.5	-3.0	-2.3	-1.5	-2.4
AA85465	cell division cycle 2 homolog, (S. pombe) lta 2	-1.0	-1.3	-1.1	1.7	2.0	-1.9	1.3	1.2	-1.0	1.5
AA859219	infectin	-1.2	-1.7	1.0	1.1	-1.2	2.2	-1.1	-1.2	1.1	-1.0
AA85974	mesoderm specific transcript	1.9	-1.3	-1.1	1.6	1.7	2.2	1.1	-1.2	1.2	-1.1
AA871814	defensin, related, cryptidin, 16	1.3	-1.0	1.4	-1.3	-1.0	2.2	-2.2	1.2	1.6	1.3
AA882227	guanine S-transferase, alpha 3	1.2	1.2	1.4	-1.6	1.3	2.2	-1.1	-1.1	1.2	-1.2
AA887076	degenerative spermatozoa homolog (Drosophila)	1.2	1.2	-1.0	1.4	1.6	2.2	1.3	1.2	1.4	-1.0
AA923491	RIKEN cDNA 160012206 gene	-2.5	1.8	2.0	1.2	2.5	-2.2	-1.0	-4.2	-1.9	-1.2
AA924317	Puic1, cornalin EST	-1.1	1.1	-1.7881	2.1	1.4	2.1	-1.2	-1.3	1.1	1.0
AA913828	hoid gene homolog, (Drosophila)	1.1	-1.9	-1.1	1.2	1.4	2.1	-2.3	-1.2	1.2	-2.4
AA108485	deoxyribonuclease I	-1.4	-1.1	1.4	1.1	1.3	2.1	-1.2	-1.8	-1.7	-1.3
AA727867	serine (or cysteine) proteinase inhibitor, clade F (alpha 2, emphysematin, pigment epithelium derived factor, member 1	1.1	-1.3	1.3	1.0	1.2	2.1	-1.6	-1.5	-1.2	1.1
AA717487	cysticotic T lymphocyte-associated protein 2 alpha	1.4	-1.8	-1.3	2.1	1.4	2.1	-1.8	-1.1	1.5	-1.4
AI595330	RIKEN cDNA 483027608, gene	-1.4	-1.0	1.2	1.3	1.3	2.1	1.3	-1.2	-1.1	1.0
AA838712	myosin, heavy polypeptide 1, skeletal muscle, adult	1.0	-1.6	1.1	1.2	1.2	2.1	-2.4	-1.4	-1.3	1.1
AA871135	myosin, heavy chain, cardiac muscle, adult	-1.1	-1.7	1.3	1.2	1.1	2.1	-1.9	-4.3	-2.1	1.4
AA726188	epithelial kinase 1	-1.3	-1.1	1.3	-1.2	1.3	2.1	-1.3	-1.5	-1.1	-1.0
AI592389	RIKEN cDNA 2700043208, gene	-1.0	-1.2	1.3	1.3	-1.2	2.1	-1.1	-1.3	1.1	1.2
AA982240	advanced glycosylation end product-specific receptor	-1.0	-1.2	-1.3	1.5	1.3	2.1	-1.1	1.2	1.0	1.1
AA851668	Aschmannase	-1.1	-1.1	1.6	1.0	1.7	2.1	-1.7	-4.5	-4.1	1.1
AA727085	erythroidin	-1.1	-1.4	-1.4	1.4	1.3	2.1	-1.5	1.2	1.1	1.2
AI420014	ESTs	-1.0	-1.1	1.3	-1.1	-1.2	2.1	1.1	-1.4	-1.2	-1.0
AA108364	ESTs, library, skin, 15, EPAGE MOUSE EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE IS TRANSFORMED BY MURINE	-1.3	1.1	1.0	-1.2	1.0	2.1	-1.8	1.0	1.1	1.1
AA674362	ESTs, Mice, brain, 15, A3772 LINE-1 hypomethylated protein 1	-1.2	-1.5	2.1	1.3	-1.3	2.1	-1.0	-1.3	-1.3	1.2
AI692747	guanine S-transferase, alpha 1 (Xa)	-1.1	-1.3	1.7	-2.1	-1.7	2.1	-1.2	-1.1	1.4	1.8
AA087338	fibroblast growth factor receptor 1	-1.2	1.0	1.4	1.5	1.5	2.1	-1.6	-1.2	1.1	1.0
AA230639	transcription factor-like protein, CDA-10	-1.2	1.7	-1.5	-1.1	-1.2	2.1	-1.2	-4.8	-1.1	-1.1
AA871841	defensin, related, cryptidin, related sequence 2	-1.0	1.3	-1.4	1.6	2.1	2.1	1.2	1.4	1.2	1.1

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AA07003 glutathione S-transferase, mu.1	11	12	10	-2.0	1.5	1.4	1.4	1.0	1.2	1.4	-1.3	-1.2
AA501707 DNA polymerase epsilon, subunit 2	-1.1	1.1	1.95228	2.0	1.4	1.5	-1.6	1.1	1.1	1.1	-1.1	1.1
AA50945 tyrosine_3-monooxygenase/hydrophen_5-monooxygenase activation protein, zeta polypeptide	-1.3	1.3	1.4	-1.1	1.2	1.5	-1.2	-2.0	-1.5	-1.2	-1.8	-1.1
AA06225 xenograftin P. pilosus.1	-2.0	1.1	-1.7	-2.5	1.0	1.5	-1.3	-1.9	-1.8	-1.9	-1.5	-1.7
AA35457 retinol binding protein 2, cellular	1.2	1.4	-1.6	-1.9	1.5	1.5	-1.3	-1.9	-1.8	-1.9	-1.1	-1.2
AA76284 ubiquitin-like 1	-1.0	-1.8	1.3	1.1	1.1	1.1	-1.7	-1.7	-1.6	-1.3	1.1	-1.1
AA67943 phosphotransferase acid phosphatase 2a	1.1	-1.1	1.4	1.2	1.3	1.3	-1.3	-1.1	1.0	1.0	1.1	-1.0
AA11080 cytochrome P450, subfamily IV B, polypeptide 1	1.0	-1.4	-1.1	-1.1	1.1	1.1	-1.9	-1.9	-1.2	-1.2	1.1	-1.1
AA871838 phospholipase A2, group IIA (rateless, synovial fluid)	-1.1	-1.0	-1.2	1.1	2.2	1.4	-1.9	-1.3	1.5	1.2	1.3	1.7
AA763276 small muscle protein, X-linked	-1.7	-1.4	1.1	1.8	1.2	1.4	-4.6	-2.5	-1.8	-1.2	-2.0	-1.5
AA38503 crystallin rich thelasma protein	1.3	1.1	-1.0	-1.6	2.3	1.5	-1.3	-1.1	1.0	-1.0	-1.0	1.1
AA13401 A kinase (PKA) anchor protein 10	1.1	1.1	-1.1	-1.0	1.3	1.3	1.0	1.2	1.1	1.1	1.2	1.1
AA95911 aquaporin 7	-1.0	-1.2	-1.0	1.8	1.3	1.4	1.1	-1.3	1.1	1.1	1.0	-1.0
AA82208 prolamine 2	-1.4	-1.8	1.3	1.4	-1.2	1.4	-1.8	-1.5	-1.7	-1.2	-1.3	-1.3
AA76873 ATPase, H <sup>+</sup> transporting, lysosomal (vacuolar proton pump) 490	-1.5	1.4	1.3	1.0	1.4	1.3	-1.1	-1.8	-1.5	-1.0	-1.9	-1.2
AA28009 isoprenyl release homeobox 3 (Drosophila)	-1.3	-1.2	-1.7	-1.5	-1.1	-1.8	1.2	-1.4	-1.2	-1.2	-1.2	-1.0
AA71181 transaldolase 1	1.0	1.1	1.1	-1.3	-1.2	-1.9	-1.0	-1.3	-1.0	1.0	-1.1	-1.0
AA14264 SEC21, gamma subunit (S. cerevisiae)	1.4	1.1	1.1	-1.4	-1.7	-1.6	-1.2	-1.3	1.1	-1.0	-1.1	-1.0
AA76474 aldol-keto reductase family 1, member B1 (aldose reductase)	1.1	-1.1	-1.2	-1.5	-1.0	-1.9	-1.1	1.0	1.1	1.0	1.1	-1.2
AA38487 ESTs	-1.0	1.1	-1.1	-1.3	-1.9	-1.6	1.0	1.0	-1.0	-1.3	1.1	1.0
W21012 lineless homolog (Drosophila)	-1.2	1.1	1.0	-1.8	-1.1	-1.8	1.1	-1.3	-1.2	-1.0	-1.3	-1.1
AA15865 RIKEN cDNA 2010306G2, gene	-1.1	-2.2	-1.5	-1.2	-1.0	-1.9	-1.1	1.1	-1.3	-1.0	-1.0	-2.4
AA121890 RIKEN cDNA 130007C21, gene	-2.0	-1.7	-1.4	-1.4	-1.4	-1.8	-1.2	-1.1	-1.7	-1.5	1.1	1.2
AA87897 carboxy ester lipase	1.5	1.5	-1.4	-2.3	-8.9	-1.6	-1.3	-1.4	-1.1	1.1	2.2	2.2
AA16864 carbonic anhydrase 4	-1.2	-1.5	-1.2	-1.4	1.3	-1.9	-1.5	1.0	-1.2	1.1	-1.2	1.2
AA15866 guanine nucleotide binding protein (G protein), gamma 10	-1.0	-1.0	-1.1	-1.3	-1.6	-1.8	1.2	-1.5	-1.3	-1.3	-1.1	-1.3
AA83482 interferon regulatory factor 2	-1.4	-1.0	-1.3	-1.5	1.1	-1.8	-1.3	-1.2	-1.3	-1.2	-1.1	-1.1
AA28002 CD32, antigen	1.1	-1.6	-1.3	1.0	-1.1	-1.9	-1.6	-1.3	-2.6	-1.1	-1.2	-1.1
W33951 platelet-activating factor acetylcholinesterase, isoform th, alpha1 subunit	1.2	-1.7	-1.1	1.2	1.3	-1.8	-1.1	1.2	1.4	1.3	1.2	1.1
AA76405 crystallin rich protein	1.0	1.4	-1.9	-1.3	1.0	1.3	-1.0	-1.4	-1.0	-1.3	1.1	1.1
AA03841 myofibrin 1	1.1	1.1	-1.2	1.1	-2.0	1.1	-1.4	-1.1	-1.4	-1.1	-1.2	-1.2
AA320722 lymphocyte antigen 6 complex, locus E	-1.1	-1.2	-1.2	-3.5	-1.1	-2.0	-1.1	-1.1	-1.1	-1.1	-1.4	1.1

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AA245754	lysosomal membrane glycoprotein 2	1.2	-1.2	1.1	-1.5	-1.6	-2.0	-1.7	-1.0	1.2	-1.1	1.1	-1.0
AA158985	heat shock protein, 70 kDa 1	1.1	-1.1	-1.0	1.2	-1.8	-2.0	-1.7	-1.1	1.1	1.1	-1.0	-1.1
AA594263	CD44a cytochrome strand	-1.4	-1.0	-2.0	-1.7	1.1	-2.0	-1.2	-1.2	-1.1	1.2	-1.1	-1.2
AA390138	RIKEN cDNA 3830401819 gene	-1.4	-10.7	-1.1	-2.0	-1.2	-2.1	-1.3	-1.2	1.5	-1.9	-1.1	-1.1
AA120076	CD24a antigen	1.3	1.2	-1.5	-2.6	-1.7	-2.1	1.1	-1.2	-1.0	-1.0	-1.4	1.1
AA522024	ESTs, highly similar to HREV, 107 PROTEIN (P, nonexposed)	1.4	1.2	1.5	-1.1	-1.3	-2.1	1.5	1.0	-1.0	-1.0	1.0	-1.2
AA159290	quantal cytosol activator 2 (quantilin 2, intestinal, heatstable)	1.0	1.0	-1.3	1.2	-2.5	-2.1	-1.5	-1.1	-1.2	-1.0	1.1	1.4
AA444443	immunoglobulin heavy chain 6 (heavy chain of IgM)	-1.2	-1.8	-1.4	1.1	1.2	-2.1	-1.9	1.1	1.0	-1.0	1.2	1.0
AA384016	complement component 1, q subcomponent c, polypeptide	1.1	-1.4	1.3	1.0	1.3	-2.1	1.1	-1.1	1.1	1.1	-1.2	-1.2
AA414831	hyposid induced gene 1	1.4	1.1	1.2	-1.3	-1.4	-2.1	1.1	-1.1	1.3	-1.1	1.1	-1.2
AA392290	RIKEN cDNA 393049815 gene	1.0	-1.3	1.1	1.6	1.3	-2.1	-1.8	1.0	1.5	1.2	1.2	1.9
AA322733	2'-5' oligoadenylate synthetase 1A	1.1	1.2	-1.1	-2.6	1.1	-2.1	-1.1	1.0	-1.2	1.1	-1.2	1.1
AA658795	ESTs	-1.0	1.4	-1.3	-1.1	1.1	-2.1	-1.1	1.3	-1.0	-1.1	1.1	1.2
AA325329	rmc0216 enhancer factor 2C	-1.3	-1.0	1.2	-1.3	-1.7	-2.1	1.2	1.2	-1.1	-1.0	-1.1	-1.2
AA138854	ESTs, weakly similar to lysophospholipase 1 (M, musculet)	-1.4	-1.6	-1.1	-1.0	-2.3	-2.1	1.1	-1.7	-1.0	1.4	-1.1	1.2
AA778905	immunoglobulin-associated alpha	-1.1	-1.8	-1.2	-1.6	-1.1	-2.1	-2.4	-1.2	-1.5	-1.3	-1.2	-1.2
AA367720	T-cell specific GTPase	1.0	-1.3	-1.2	-1.6	-1.1	-2.1	1.2	-1.4	-1.4	-1.2	-1.0	-1.0
AA676094	elastase 2	-2.3	1.4	-1.2	-2.7	-2.1	-2.2	-1.7	-1.9	-4.0	-1.4	-1.2	-1.4
AA123007	2'-5' oligoadenylate synthetase-like	1.1	-1.4	-1.3	-2.2	-1.1	-2.2	-1.1	1.3	-1.1	-1.1	-1.1	-1.1
AA237793	rat nonreleasing, lipid-derived, mouse homologue 1	-2.1	1.4	-1.3	-3.9	-1.8	-2.2	1.0	-1.4	-2.7	-1.2	-1.2	-1.2
AA686697	rat intestinal adipose proteinase	1.1	1.3	-1.2	1.7	1.1	-2.2	1.3	1.5	1.2	1.0	1.6	1.3
AA375752	transglutinin	1.1	-1.1	-1.2	-1.5	1.1	-2.2	-1.6	-1.2	-1.4	1.0	-1.7	-1.1
AA325697	lymphocyte antigen 6 complex	1.3	-1.1	1.6	-1.3	1.1	-2.2	-1.3	-1.1	1.4	1.1	1.1	-1.1
AA327943	sperm specific antigen 1	1.0	-1.0	1.1	-1.1	-1.2	-2.2	1.0	1.0	1.1	1.1	1.0	1.0
AA602916	ESTs	-1.2	-1.1	1.3	-1.5	-1.9	-2.3	-1.4	-1.4	-1.2	-1.2	-1.5	-1.1
W62505	uracil transferase, mitochondrial	1.1	-1.0	1.3	-1.7	-1.3	-2.3	-1.2	-1.3	-1.0	-1.3	-1.2	-1.2
AA360652	histocompatibility 2, class II, locus DMe	-1.3	1.2	-1.2	1.2	1.1	-2.3	1.0	-1.1	-1.3	-1.0	-1.0	-1.1
AA359768	caseinase 7	-1.0	1.0	-1.0	-1.0	-1.0	-2.3	-1.4	-1.2	-1.2	1.0	-1.0	-1.1
AA027890	0-6-methylguanine-DNA methyltransferase	-1.2	1.2	-1.6	-1.9	1.3	-2.3	1.0	-1.1	-1.1	-1.2	-1.1	-1.1
AA61911	mus musculus, clone MGC-8727, mRNA, complete cds	-1.1	-2.0	-1.8	-1.0	-1.8	-2.3	-1.5	-2.4	-1.4	-1.4	-1.4	-1.4
AA62574	tail-anchored	1.8	1.5	-1.2	-1.4	-2.7	-2.3	-1.2	2.3	-1.2	-1.1	1.0	1.3
W15001	CD52 antigen	1.1	-1.7	1.2	1.1	1.1	-2.3	-1.2	-1.2	2.5	1.1	-1.0	-1.0
AA619407	pancreatitis-associated protein	1.7	1.6	-1.6	1.2	1.2	-2.4	-1.1	-1.3	1.0	-1.2	1.3	1.1

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AA575501 ESTs	-14	22	10	-13	12	-24	13	-16	-15	-12	-13	-11
AA684403 ESTs	-14	17	-23	-20	23	-24	15	-10	-13	-13	-11	-11
AA680722 <i>ap505046</i> complement related protein of 90 kDa	-13	-12	-10	-13	10	-24	-20	-11	-15	-11	-13	-15
AA690349 glutathione peroxidase 2, pseudogene 1	-13	-10	12	-18	11	-24	-25	-15	11	-11	-15	-15
W09188 calcium binding protein A5 (calgadin)	12	-12	-22	-16	-18	-24	11	11	10	12	-12	10
A036002 carboxic anhydrase 3	11	-13	23	-15	11	-24	-11	-21	-13	-12	-16	-15
AA592295 immunoglobulin chain, chain	12	-15	-14	17	-22	-24	-19	-11	13	15	14	-13
A036624 <i>mtc2000</i> cytochrome oxidase (cytochrome oxidase) 3	13	13	-12	22	152102	-24	12	14	13	11	13	15
AA144778 <i>M.musculus</i> mRNA (3C10) for JPA V2-Jheery chain	-13	10	-16	27	-20	-24	-11	-14	15	20	11	16
AA021068 proteasome (prosome, macropain) subunit, beta type 10	-11	12	12	-11	-11	-25	-10	-13	-11	-12	11	-12
AA51862 RIKEN cDNA 0910001A16 gene	18	13	-11	-26	-17	-26	12	-13	-24	-13	-11	-13
AA380048 <i>lyt1</i> 4	17	18	11	-18	-168	-28	18	-15	-25	-11	-13	-12
AA390007 RIKEN cDNA 251002A12 gene	-10	-11	-17	-13	-12	-26	-11	-12	11	10	11	-11
AA055045 proteasome (prosome, macropain) subunit, beta type 9 (large, multi-subunit, P30828.2)	-12	-14	-11	-11	-11	-26	-11	-11	-11	-11	-10	-13
AA650322 calpain 1	-12	-18	-12	-10	-25	-26	11	-14	-12	11	-11	-17
AA272405 <i>dhfr</i> cytochrome reductase	-12	11	11	-16	11	-26	24	13	-11	14	-13	-13
AA26519 ESTs Moderately similar to F3H1_MOUSE_gpf-2/KFRU2-6-PAASE LIVER ISO2XME (M.musculus)	-14	11	10	-12	-26	-12	-13	11	11	-11	-11	-11
AA792277 lymphocyte antigen 8 complex, locus C	-16	15	-21	-19	17	-27	15	-11	-12	-13	-12	-12
AA040400 claudin 4	14	-15	12	11	15	-27	-11	12	-16	11	-11	-14
AA26566 <i>hsc70</i> heat shock protein 70, class II antigen E alpha	-12	-10	11	10	13	-27	-28	-11	-11	-11	-13	10
W11710 small inducible cytokine A21s (haudine)	14	-16	-12	-11	-19	-27	-20	-14	-13	14	-12	-23
AA677694 <i>ap505046</i> complement related protein of 90 kDa	11	-11	-11	-20	-11	-27	-16	-11	-10	10	-10	12
U008261 inhibitor of DNA binding 1	-12	-11	-11	11	12	-28	-12	-14	-11	11	-12	-12
AA157238 <i>hsc70</i> heat shock protein 70, class II, locus Mh1	-11	12	-11	14	14	-28	12	10	12	-24	13	13
AA272406 <i>ap505046</i> complement related protein of 90 kDa	14	-12	-11	-11	-19	-29	-28	-16	-10	14	-10	-27
AA4618184 immunoglobulin kappa chain variable 20 (V20, family)	12	-17	-11	15	10	-29	-12	12	-17	11	10	-11
AA752745 <i>hsc70</i> heat shock protein 70, class II, antigen E beta	-14	11	-21	-18	13	-30	12	-12	-11	-13	-10	-12
AA292628 ESTs	13	-14	-20	14	-17	-30	-31	-13	12	13	14	-17
AA371265 <i>hsc70</i> heat shock protein 70, class II, locus Mh1	13	-16	-15	-10	-21	-31	-22	-13	-13	-11	-25	-11
AA159240 immunoglobulin kappa chain variable 20 (V20)	18	-15	-10	-12	-19	-32	-19	-10	-12	-10	-11	-14
AA754938 immunoglobulin heavy chain 4 (heavy chain of IgM)	17	-23	-12	-28	-28	-33	-19	-19	-11	-11	-12	-11
AA793338 <i>hsc70</i> heat shock protein 70, class II, antigenic	11	12	-11	-21	113744	-33	-11	11	-11	11	11	13
AA072934 RIKEN cDNA 090418M05 gene												

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W17930 small inducible cyclin A21a (leucine)	-1.2	1.0	-1.4	-1.2	1.2	-3.3	-1.3	-1.0	-1.2	-1.5	-1.2
AA242406 CEK-related cell adhesion molecule 1	-1.1	-1.1	1.0	1.4	1.5	-3.4	1.2	-1.0	-1.1	-1.0	1.2
AB27143 CST3	-1.0	-1.1	-1.1	-1.3	-2.5	-3.6	1.2	-1.1	-1.2	-1.1	-1.1
AA250037 proteasome (prosome, macropain) subunit, beta type 8 (large multi- functional protease 7)	1.1	-1.5	1.1	-1.9	1.0	-3.6	-1.5	-1.2	-1.1	1.2	-1.0
W15919 hemoglobin, beta adult major chain	1.5	-1.2	1.2	-2.9	1.3	-3.7	1.4	-1.2	-1.0	-1.7	-1.6
AA759679 leucosialin invariant chain	-1.0	-1.8	-1.6	-1.9	1.5	-3.7	-2.8	-1.0	-1.9	-1.0	-1.3
AA750409 silyltransferase 7, (alpha-N-acetylneuraminy 2,3-bellagachoxyl-1,3)- N-acetyl galactosaminide alpha-2,6-silyltransferase) P	-1.0	-1.1	1.0	1.2	1.3	-3.9	1.2	-1.1	-1.4	1.0	-1.1
AB656448 small proline-rich protein 2A	-1.0	-1.1	-1.4	-1.3	-5.5	-3.9	1.0	-1.2	-1.2	-1.1	-1.5
AA651844 amylase 2, pancreatic	3.1	1.1	-1.2	-2.8	-32.0	-4.0	2.0	-1.2	-4.4	-1.1	-1.2
A936257 calbindin-D9K	-2.2	-1.3	1.2	1.5	-53.5	-4.1	1.0	-1.2	-1.1	-1.2	1.4
AA066763 hemoglobin, beta adult major chain	1.3	-1.2	1.4	-4.0	1.1	-4.2	3.5	-1.1	-1.3	1.5	-1.8
AA100771 hemoglobin, beta adult major chain	1.3	-1.4	1.2	-3.0	-1.1	-4.3	3.2	1.1	-1.3	1.8	-1.7
AA158011 histocompatibility 2, class II antigen A, alpha	-1.1	-1.3	1.0	1.3	-4.5	1.2	1.1	-1.9	-1.3	-1.0	-1.2
AA467816 cytochrome	1.3	-1.8	-1.1	-1.6	-6.1	-5.0	1.5	-1.2	-1.3	-1.2	1.5
AA177025 beta muscle 10 day old male zebrafish cDNA, RIKEN full- length cDNA clone, clone:10050A17, full insert sequence	1.9	-1.1	-1.2	-2.7	-28.5	-5.2	2.1	-1.6	-2.9	1.2	-1.1

TABLE 2

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COLON



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intestine	spl	panc	liv	stom	int	col	br	lung	blad	kidn	plut	nam
Description	PL- 48_BDEx	PL- 120_BDEx	PL- 165_BDEx	PL- 180_BDEx	PL- 185_BDEx	PL- 190_BDEx	PL- 195_BDEx	PL- 200_BDEx	PL- 205_BDEx	PL- 210_BDEx	PL- 215_BDEx	PL- 220_BDEx
A0159407 pancreatic-associated protein	1.2	19.5	-1.9	1.2	4.4	-2.4	-1.1	-1.3	1.0	-1.2	1.3	1.1
A0272882 cytochrome P450, 2a25	1.5	-1.2	1.3	-1.1	4.0	2.5768	-1.1	-2.2	1.2	1.1	1.0	1.3
W65363 peripheral myelin protein, 22 kDa	1.5	10.5383	1.4	1.1	3.5	-1.0304	1.2	1.1	1.3	1.2	1.1	-1.2
A0107032 guanylate cyclase, activated 2P, (rodna)	-1.2	-1.3	1.1	-1.1	3.1	3.7	-1.5	1.7	-1.9	-1.2	-1.3	6.5
A0119804 aminotetras	-1.1	1.065094	1.1	1.2	3.0	1.27974	-1.2	1.0	1.1	1.1	-1.1	1.5
A0106713 RIKEN cDNA 0610010C5, gene	-1.1	-1.1	1.1	-1.0	2.8	1.6	1.0	1.0	1.3	1.6	-1.1	1.0
A0321162 diaphidase 1, (mna)	1.3	-1.3	-1.4	1.3	2.9	1.1	-1.5	-1.3	-1.1	1.0	1.0	-1.3
A0871935 phenolphthalein A2_group IIA (phenolphthalein) (lidi)	-1.1	-1.0	-1.2	1.7	2.8	1.2	-1.9	-1.3	1.5	1.2	1.3	1.7
A065534 RIKEN cDNA 1110022J15, gene	1.6	1.3	1.1	-1.4	2.7	1.4	-1.1	1.1	-1.0	1.3	-1.2	-1.2
A065534 cytochrome P450, 2b5, phenobarbital-inducible, ypo_#	-1.1	-1.4	1.5	1.3	2.8	3.6	-1.3	1.1	1.3	1.2	1.1	1.2
W11894 guanylate cyclase, activator 2, (guanylin_2, longshino) (metastable)	1.0	1.0	-1.3	1.2	2.3	2.1	-1.5	-1.1	-1.2	-1.0	1.1	1.4
A0355330 cytochrome P450, 2b13, phenobarbital-inducible, ypo_5	1.4	-1.1	2.0	1.0	2.8	2.8268	1.0	1.1	1.2	-1.2	1.1	1.4
A0242301 serine protease, inhibitor, Kex1 type 3	1.5	1.8	-1.4	1.1	2.5	-1.0	-1.8	1.2	-1.2	-1.0	1.0	2.6
A0515327 sphingolipase, phosphatase, ypo_1	1.1	1.1	1.4	1.2	2.4	1.7	1.3	1.2	-1.0	1.3	1.0	-1.0
A063765 metallothionein_1	1.0	1.1	2.5	1.2	2.4	1.5	1.2	-1.8	-1.3	1.2	-1.9	-1.2
A0522935 sphingomyelinase 1, ypo_1	-1.8	-1.5	1.1	-2.4	2.1	2.4	-1.9	-1.0	-1.2	-2.1	-2.5	-1.8
A0671063 dectin-related cysteine, related sequence 7	1.2	-1.4	-1.6	1.1	2.3	1.3	-1.2	-1.5	-1.1	-1.5	1.1	1.2
A073433 guanylate aminopeptidase	1.3	1.1	1.1	1.3	2.3	-1.0	1.3	1.1	1.5	1.0	1.2	-1.1
A068198 dectin-related cysteine, related sequence 10	-1.0	-1.1	-1.7	2.0	2.3	1.5	1.2	1.2	1.2	1.6	1.1	1.6
A034338 glycosylphosphatidylinositol-specific phospholipase D1	1.1	-1.3	1.2	-3.4	2.3	-1.5	-2.0	-1.2	-1.3	1.2	-1.8	-1.8
A069225 eelenopterin P, plasma_1	1.2	1.4	1.2	-1.7	2.3	1.4	1.5	-1.2	-1.1	1.2	-1.6	-1.1

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TABLE 2

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A0024217	Public domain EST	-2.5	1.6	2.0	1.2	2.3	2.2	1.0	4.2	-1.9	-1.2	-2.3	1.1
A0162450	RIVEN cDNA 1200010111 gene	-1.0	1.1	-1.1	-1.1	2.1	1.0555	-1.4	-1.0	1.1	-1.2	-4.2	1.1
A339593	cytochrome b7b intestinal protein	1.3	1.1	-1.0	-1.6	2.5	1.5	-1.3	-1.1	1.0	-1.0	-1.0	1.1
A412211	guanine nucleotide binding protein alpha 11	-1.0	1.0	-1.0	1.3	2.3	1.2	1.2	1.0	1.2	1.1	1.0	1.0
A416344	histone deacetylase 7	1.2	1.8	1.9	-1.2	2.2	1.28947	1.7	1.5	1.0	1.4	-2.2	1.0
A2328419	P. glycoprotein 2	1.0	-1.2	-1.0	-1.1	2.2	1.0	1.0	1.0	1.1	-1.0	-4.2	1.3
A108538	ESTs, Weakly similar to CATC MOUSE COLLAGEN ALP	-1.1	-1.1	-1.0	-1.1	2.2	1.7844	-1.5	1.0	-3.2	1.4	-4.1	1.0
A210237	HA [XII] CHAIN PRECURSOR [M.musculus]	-1.0	-1.1	-1.1	-1.1	2.2	1.1	-1.5	1.1	1.1	-1.1	-1.1	-1.2
A470502	actin, alpha 1, skeletal muscle	-1.5	-1.4	1.7	1.5	2.2	1.64011	-1.3	-8.0	-1.0	-1.1	1.2	1.1
A457338	cycloheximide P450, steroid inducible 3a11	-1.3	-1.3	1.0	-1.3	2.1	1.824	1.1	1.3	1.1	1.1	1.1	-1.0
A338758	ESTs	-1.0	1.3	-1.4	1.6	2.1	2.0	1.2	1.4	1.2	1.1	1.5	1.5
A4571841	defensin related cryptdin, related sequence 2	-1.5	-1.1	-1.0	1.8	2.1	1.8	-1.0	-1.2	1.2	-1.1	1.1	1.0
A371410	defensin related cryptdin 5	-1.1	1.0	-1.0	1.0	2.0	1.5	1.3	1.3	1.2	1.4	1.0	-1.0
A4210237	Mus. musculus, clone MGC34377, mRNA, complete cds	-1.3	-1.1	1.3	1.1	2.0	1.2	-1.2	1.4	1.0	-1.0	1.0	1.1
A1552037	IQ motif containing, GTPase activating protein_1	-1.3	1.0	-1.0	1.1	2.0	1.2	1.3	1.0	1.2	-1.1	1.1	-1.5
A4168427	Mus. musculus, germline, immunoglobulin, gamma, constant, J	1.1	-1.2	1.1	-1.1	2.6	-1.3	1.0	1.2	1.1	1.1	-2.3	1.1
A478138	actin, gamma 2, smooth muscle, embryonic	1.0	-1.1	-1.1	-1.0	2.0	1.4	1.2	-1.1	-1.0	-1.2	-4.4	1.6
A4239727	ATP-binding cassette, sub-family, B (MOT/TAP), member 1	1.7	1.8	-1.4	3.1	2.0	1.31548	-1.3	2.3	2.0	1.8	2.2	2.1
A449830	chlorine kinase	1.4	1.1	1.2	-2.1	2.0	1.8	-1.0	-1.1	-1.0	1.3	-1.1	-1.2
A594147	beta-2 microglobulin	-1.4	1.7	-2.3	-2.0	2.8	2.3	1.5	-1.0	-2.3	-1.3	-1.1	-1.1
A4694403	ESTs	-1.0	-1.3	-1.1	1.7	2.0	2.2	1.9	1.3	1.2	-1.0	1.5	1.8
A469210	Insectin	1.3	1.6	-1.4	2.5	2.0	1.2077	-1.1	1.9	1.6	1.2	1.6	1.9
A467595	ESTs	1.3	1.7	-1.0	-1.5	2.0	1.2	-1.4	1.1	1.2	1.3	1.2	1.0
U54593	guanine-7-S-transferase, mu 2	-1.0	-1.0	-1.2	1.8	1.9	-1.4	1.2	1.0	1.2	1.1	-2.1	1.5
A4013726	cathepsin J	1.5	1.9	-1.3	3.8	1.4	1.01549	-1.1	2.2	2.1	1.0	2.5	2.5
A1548524	RIVEN cDNA 0510041509, gene	-1.2	1.2	1.1	1.1	2.1	1.1	1.1	-1.2	-1.0	-1.1	-1.5	1.1
A152639	ESTs, Weakly similar to MIA MOUSE MELANOMA DERIVED GROWTH REGULATORY PROTEIN PRECURSOR [M.musculus]	1.3	-1.3	1.1	-1.1	1.6	1.48772	-1.2	1.2	1.4	1.1	1.0	1.1
A4450725	membrane metallo endopeptidase	-1.0	1.0	-1.3	2.0	1.9	-1.0	-1.8	-1.1	1.0	-1.6	1.4	1.1
A4870247	myoglobin regulated protein, profilin 3	-1.1	-1.2	1.0	1.3	1.0	-1.3	-1.0	1.1	-1.2	1.1	-1.1	-1.1
A1893437	transglutaminase 2, C polypeptide	-1.1	-1.0	1.2	1.4	1.7	1.32031	-1.1	-1.2	1.1	1.6	1.2	-1.3
A036411	glutathione transferase, gamma	1.3	1.6	-1.0	-1.6	1.8	-1.0	-1.2	-1.2	-1.1	-1.1	-1.3	-1.2
A4619767	ornithine decarboxylase, embryonic	1.1	-1.0	1.3	1.1	1.6	-1.4	1.3	1.1	1.0	1.1	-1.1	-1.1
A4106523	heosaminidase, B	1.1	-1.0	1.3	1.1	1.6	-1.4	1.3	1.1	1.0	1.1	-1.1	-1.1

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TABLE 2

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W14224 N-myristeam regulated 1	1.1	1.0	1.0	1.1	1.0	1.2	1.1	1.6	1.0	1.3	2.1
A652440 actin, alpha 2, smooth muscle, aorta	-1.0	1.2	-1.3	-1.1	1.3	-1.3	-1.6	1.1	1.1	1.0	-1.2
W08474 myosin heavy chain 2	-1.2	-2.2	-2.1	1.2	1.1	1.3	1.1	-1.8	-1.1	1.6	1.8
A6521963 aspartyl aminopolysaccharide	1.0	1.0	1.1	-1.2	1.5	1.8	1.1	-1.0	1.0	1.3	-1.2
W13527 synchrotron P450_2j6	1.4	-1.0	1.1	-1.4	1.4	2.9	1.3	-1.3	1.2	-1.0	1.4
A4113490 transferrin receptor	1.4	-1.3	1.2	-1.0	1.3	1.1	1.2	1.2	-1.3	1.5	1.5
A1554083 Mus_musculosa_deltoides COMP_protein (Comp_mRNA)_com	-1.1	-1.3	1.1	1.4	-1.9	-1.14099	-1.6	1.2	-1.0	-1.2	-1.3
A4028420 small profilin-rich protein 1A	1.3	-1.7	-1.4	-1.1	-1.9	-1.2	-1.9	-1.2	1.0	-1.1	1.3
A245987 ESTs	-1.01244	-1.30375	1.1	1.29885	-1.9	1.12119	-1.6843	-1.02333	1.2	1.26207	1.85154
A180129 proteasome (prosome, macropain) subunit, alpha type 2	1.1	1.0	1.3	-1.4	-1.9	-1.6	1.1	-1.2	1.2	1.0	-1.3
A155662 nuclear receptor subfamily 5, group A, member 2	-1.3	1.2	-1.1	-1.1	-1.9	-1.40144	-1.0	-1.4	-1.2	-1.5	-1.2
A155662 nuclear receptor subfamily 5, group A, member 2	1.0	-1.4	-1.1	-1.1	-1.9	-1.1	1.4	1.2	-1.4	-1.5	-1.0
A050516 ESTs	-1.2	-1.1	1.3	-1.5	-1.9	-2.3	-1.4	-1.4	-1.2	-1.5	-1.1
A551934 ESTs	-1.5	-1.5	-1.4	1.1	-1.9	-1.03856	-1.9	-1.2	-1.1	-1.5	1.0
A157053 RIKEN cDNA 270084F01, gene	-1.0	-1.6	-1.0	-1.1	-1.9	-1.1	1.2	1.1	-1.3	-1.4	1.0
A1784319 ESTs	-1.1	-1.1	1.3	-1.7	-1.9	-1.3	-1.2	-1.4	-1.3	-1.0	-1.1
A443804 ESTs	-1.1	-1.1	-1.1	-1.2	-1.9	-1.0	-1.0	-1.0	-1.2	-1.4	-1.1
A474486 immunoglobulin heavy chain 6 (heavy chain of IgM)	1.6	-1.5	1.0	-1.2	-1.9	-3.2	-1.9	-1.0	-1.2	-1.0	-1.1
W09196 calcium binding protein A8 (calyculin)	1.2	-1.2	-1.2	-1.6	-1.9	-2.4	1.1	1.1	1.9	1.2	-1.2
A4967624 arginine vasopressin	1.4	-1.6	-1.2	-1.1	-1.9	-2.7	-2.0	-1.4	-1.3	-1.4	-1.2
A4968194 immunoglobulin kappa chain variable 20 (V20 family)	1.4	-1.2	-1.4	-1.1	-1.9	-2.9	-2.6	-1.8	-1.0	1.4	-1.0
A451676 ESTs	-1.3	-1.3	-1.0	1.3	-1.9	1.14107	-1.0	-1.2	-1.2	-1.3	-1.0
A1780465 RIKEN cDNA 3110071D0, gene	1.1	-1.1	1.2	-1.1	-1.9	-1.90429	1.2	-1.1	-1.1	1.0	1.3
A056562 RIKEN cDNA 281047H19, gene	-1.0	-1.5	-1.1	-1.1	-1.9	-1.0	-1.0	-1.2	-1.5	-1.1	-1.2
A627053 ESTs	-1.3	-1.1	-1.1	1.1	-1.9	-1.03772	1.3	-1.0	-1.1	-1.4	1.1
A407643 ESTs (Weakly similar to S12207, hypothetical protein JM.musculus)	1.2	-1.2	-1.1	-1.2	-1.9	1.1	1.0	1.1	-1.1	-1.3	1.1
A536309 RIKEN cDNA 2210410L06, gene	-1.8	-1.8	-1.4	-2.1	-1.9	1.1	-1.5	-2.0	-1.6	-2.1	-1.5
A418366 translocase of ERB-2.1	-1.0	-1.2	1.3	-2.0	-1.9	-1.1	1.1	-1.2	-1.1	-1.0	-1.2
A414465 ESTs	-1.2	-1.3	-1.0	1.0	-1.9	1.2	1.0	-1.0	-1.2	-1.3	1.0
A4559377 heat shock protein, 66 kDa 1	1.4	1.0	-1.3	-1.9	-1.9	-1.5	1.4	1.3	1.2	-1.0	-1.3
A4559377 heat shock protein, 66 kDa 1	-1.0	-1.4	1.1	-1.2	-1.9	-1.1	1.1	1.1	-1.0	1.0	-1.1
A4559377 heat shock protein, 66 kDa 1	1.0	-1.5	-1.1	-1.3	-1.9	-1.2	1.3	1.2	-1.1	-1.1	-1.1
A4559377 heat shock protein, 66 kDa 1	-1.0	-1.4	1.1	-1.2	-1.9	-1.1	1.1	1.1	-1.0	1.0	-1.1
A4559377 heat shock protein, 66 kDa 1	1.0	-1.5	-1.1	-1.3	-1.9	-1.2	1.3	1.2	-1.1	-1.1	-1.1

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TABLE 2

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AA79842, proteasome, (prosome, macropain) subunit, alpha_type_3	12	-10	14	-13	-19	-15	11	-11	12	-11	11	-12
AI06604, complex testis expressed_1	11	-16	-10	13	-16	14	11	14	-10	-11	13	-10
AI03640, ESTs	-10	11	-11	-13	-19	-19	10	-10	-13	11	-10	-10
AI38161, gamma-glutamyl carboxylase	-10	-11	-11	-13	-19	-19	10	-10	-13	11	-10	-10
AA42742, ESTs, highly similar to AF01622_1 p1D, finger protein_3	-11	-13	-10	-12	-19	-19	10	-10	-13	11	-10	-10
AI18494, ESTs	-15	-13	-12	11	-19	-14	-12	11	-11	-12	-11	-11
AA29969, ESTs	-12	-12	-11	11	-19	-14	-12	11	-11	-12	-11	-11
W6457, interferon (alpha and beta) receptor	-10	-14	-11	-12	-19	-14	-12	11	-11	-12	-11	-11
AI28606, ESTs, weakly similar to S12207, hypothetical protein [M.musculus]	10	-15	10	-11	-19	-13	11	12	-10	-12	10	-13
AA175747, RIKEN cDNA, 2910311.0, gene	-11	-14	-11	-11	-19	-13	11	-10	-11	-14	10	-11
AA56375, DNA segment, Chr. 8, ERATO Dcl 239, expressed	-12	-11	11	-10	-19	-13	11	-11	-13	11	-10	-10
AA14730, NCK-associated protein 1	12	-11	10	-16	-19	-12	12	11	12	11	11	11
AA27692, ESTs, weakly similar to R6A, MOUSE GROWTH FACTOR RECEPTOR-BINDING PROTEIN 10 (M.musculus)	-13	-18	-12	-11	-19	-13	-13	12	11	-11	13	13
AI38300, ESTs, moderately similar to S12207, hypothetical protein [M.musculus]	-10	-12	-12	-11	-19	-13	-13	12	11	-11	13	13
W24620, keratin 28	12	11	-11	-14	-19	-13	-13	12	11	-11	13	10
AI59238, ESTs	10	-17	-11	-14	-19	-13	-13	12	11	-11	13	10
AA77390, ESTs, moderately similar to S1227, hypothetical protein [M.musculus]	-10	-11	10	-11	-19	-13	-13	12	11	-11	13	10
AA47755, thymus expressed acidic protein	-13	-16	-10	-11	-19	-13	-13	12	11	-11	13	10
AA91354, cyclin T1	-14	-12	-12	-16	-19	-13	-13	12	11	-11	13	10
AI68328, ESTs	-12	-14	-13	-12	-19	-13	-13	12	11	-11	13	10
AA44751, double C2, gamma	-12	-13	-13	-14	-19	-13	-13	12	11	-11	13	10
AA69638, ESTs, highly similar to S12207, hypothetical protein [M.musculus]	10	-11	10	-13	-19	-13	-13	12	11	-11	13	10
AA73741, DNA segment, Chr. 12, ERATO Dcl 804, expressed	12	-14	-13	-14	-19	-13	-13	12	11	-11	13	10
AA61089, RIKEN cDNA, 670304.C05, gene	-11	-10	11	-12	-19	-13	-13	12	11	-11	13	10
AS93019, ESTs, weakly similar to apolipoprotein F (F.hisialis)	-11	-15	12	-11	-19	-13	-13	12	11	-11	13	10
AB14000, ESTs	-11	-12	10	-11	-19	-13	-13	12	11	-11	13	10
AA74176, ESTs, moderately similar to SPA-1 like protein p1794 (R.norvegicus)	-10	-20	-12	-12	-20	-12	-12	13	-13	-13	11	-11
AI166376, ESTs	-11	-17	-12	-11	-20	-12	-12	13	-13	-13	11	-11
AA69612, RIKEN cDNA, 483116.520, gene	-11	-13	11	-11	-20	-12	-12	13	-13	-13	11	-11
AA17238, ESTs	-12	-12	10	11	-20	-12	-12	13	-13	-13	11	-11
AA25351, adrenocort, desminase	11	11	-11	11	-20	-12	-12	13	-13	-13	11	-11

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TABLE 2

AA415510 ESTs	-1.0	-1.4	-1.1	-1.3	-2.0	-1.1	1.2	1.1	-1.2	-1.2	-1.1	-1.1
AA47194 EST	-1.1	-1.3	-1.2	-1.2	-2.0	1.0	-1.2	1.1	-1.2	-1.5	-1.0	-1.2
AA52448 ESTs, Weakly similar to NEDD_MOUSE_NEDD-4 PROTEIN (M.musculus)	1.8	-1.2	-1.0	-1.1	-2.0	1.2	1.0	1.3	-1.1	-1.3	1.1	-1.2
A120315 splicing factor, arginine/serine-rich 6 (SRP40_HRS)	1.8	-1.4	1.2	-1.1	-2.0	-1.0	-1.3	-1.0	1.1	-1.2	-1.1	-1.4
AA536920 ESTs	-1.1	-1.3	1.2	-1.1	-2.0	1.0	1.2	1.1	-1.2	-1.2	-1.0	-1.3
AA62640 cDNAs, Weakly similar to AF030806.1_bryodominense-3883 (vector protein, H.sapiens)	1.1	-1.5	1.0	-1.1	-2.0	1.1	-1.1	1.1	-1.1	-1.2	1.0	-1.3
AA49387 tumor rejection antigen, ga68	1.3	1.4	1.5	-1.9	-2.0	-1.4	1.2	-1.1	1.2	-1.1	1.1	-1.0
AA19315 ESTs, Moderately similar to S12207_hypothetical protein [M.musculus]	-1.5	-1.1	-1.2	-2.0	1.0	1.2	1.2948	1.1	-1.2	-1.6	-1.0	-1.2
AA59850 ESTs	-1.0	-1.1	1.1	-1.1	-2.0	-1.1	-1.2	1.1	-1.1	-1.4	1.0	1.0
AA383009 ESTs	-1.4	-1.3	-1.1	-1.3	-2.0	-1.42866	-1.0	-1.1	-1.3	-1.4	-1.1	-1.2
A035637 serine/arginine-rich protein, specific kinase 2	1.0	-1.6	-1.0	-1.1	-2.0	-1.0	1.0	-1.1	-1.2	-1.4	-1.0	-1.1
A175610 ESTs, Moderately similar to S12207_hypothetical protein [M.musculus]	-1.1	-1.0	1.1	1.1	-2.0	1.0	-1.4	-1.1	-1.0	-1.0	-1.2	-1.1
AA148478 M.musculus, mRNA (3C10) for [6A_V-D-Heavy chain	1.0	-1.3	-1.0	-1.1	-2.0	1.1	-1.1	-1.0	-1.1	-1.3	-1.1	-1.2
AA307221 ESTs, Weakly similar to NEDD_MOUSE_NEDD-4 PROTEIN (M.musculus)	-1.1	-1.2	-1.0	-1.0	-2.0	-1.0	-1.2	1.1	1.0	-1.2	1.1	1.0
AA549413 ESTs, Weakly similar to T44158_hypothetical protein DNF Z1454132.1 (H.sapiens)	1.1	-1.7	1.0	-1.1	-2.0	1.0	1.0	1.1	-1.1	-1.2	1.1	-1.2
AA82929 ESTs	-1.1	-1.4	-1.0	-1.1	-2.0	-1.0	-1.2	1.1	-1.2	-1.2	-1.0	-1.1
AA52745 M.musculus, clone MGC3888, mRNA, complete cds	1.1	1.1	1.1	-2.0	-2.0	1.1	-1.2	-1.5	-1.2	-1.4	-1.3	-1.1
AA49008 anterior gradient 2 (Xenopus laevis)	1.4	1.1	-1.4	-1.7	-2.0	-1.4	1.4	-1.0	-1.0	-1.0	-1.0	-1.2
AA82934 ribosomal protein, S24	1.3	1.1	1.3	-2.1	-2.0	-1.1	1.3	-1.2	1.2	-1.4	-1.1	-1.2
AA650338 M.musculus, mRNA, for erythroid differentiation regulator, pefel	-1.0	-1.0	-1.2	-1.5	-2.0	-1.3	-1.7	-1.3	-1.3	-1.6	-1.2	-1.2
AA619114, polr1a, gene family, V1 protein	1.1	1.0	1.0	-1.2	-2.0	-1.4	-1.5	1.4	1.1	-1.0	1.1	-1.0
AA62655 ribosomal protein, L25, member 2	-1.2	-1.4	-1.0	-1.3	-2.0	1.0	-1.1	-1.1	-1.2	-1.3	-1.1	-1.1
AA549440 ESTs	1.1	-1.4	-1.0	-1.0	-2.0	1.0	1.4	1.3	-1.1	-1.4	1.2	1.1
AA69387 RIKEN cDNA, 3010002H3, gene	1.3	-1.1	1.0	-1.1	-2.0	-1.1	1.4	1.3	-1.1	-1.7	-1.2	-1.2
AA69045 ESTs	-1.1	-1.5	-1.1	-1.3	-2.0	-1.0	-1.0	-1.0	-1.0	-1.3	1.0	-1.2
AA47445 ESTs	1.3	-1.5	-1.1	1.3	-2.0	-1.1	1.3	-1.1	-1.1	-1.3	1.2	-1.1
AA444072 RIKEN cDNA, 251001A17, gene	-1.1	-1.0	1.1	-2.3	-2.0	-1.1	1.3	-1.1	1.2	-1.4	1.0	-1.2
AA473072 heterogenous nuclear ribonucleoprotein, H	1.5	-1.2	1.2	-1.8	-2.0	-1.17965	-1.2	1.0	1.1	-1.5	-1.1	1.1
AA37109 ESTs	-1.1	-1.3	1.1	-1.1	-2.0	-1.2	1.3	1.1	-1.1	-1.1	1.1	-1.2

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A483620 ESTs, Moderately similar to S12207_hypothetical protein 1 (Mus musculus)	1.0	-1.3	-1.0	-1.1	-2.0	-1.5	-1.1	-1.1	-1.1	-1.3	-1.0	-1.2
A391001 Public domain EST	-1.2	-1.3	-1.0	-1.0	-2.0	-1.1	-1.0	-1.1	-1.0	-1.1	-1.4	-1.0
A4576047 ESTs	-1.3	-1.4	-1.1	-1.1	-2.0	-1.3	-1.2	-1.1	-1.4	-1.1	-1.0	-1.0
A450530 ESTs	-1.1	-1.3	-1.1	-1.3	-2.0	-1.2	-1.0	-1.1	-1.3	-1.4	-1.1	-1.1
A4538798 RIKEN cDNA 111002806 gene	1.2	1.0	1.5	-1.3	-2.0	-1.3	-1.1	-1.2	1.0	-1.1	-1.1	1.0
A464191 CDC-19a kinase	1.5	-2.1	-1.3	-1.1	-2.0	-1.4	-1.3	-1.4	-1.4	-2.1	1.4	1.2
A464581 ESTs, Highly similar to CRH1 (H. sapiens)	-1.2	-1.7	-1.1	-1.4	-2.0	-1.4	-1.2	-1.0	-1.4	-1.4	-1.0	-1.1
A356183 Public domain EST	1.0	-1.1	1.0	1.1	-2.0	-1.0	-1.4	-1.1	-1.0	-1.2	1.1	-1.1
A4871433 ESTs	-1.2	-1.8	-1.1	-1.2	-2.0	-1.3	-1.1	-1.1	-1.2	-1.4	-1.0	-1.2
A484082 ESTs, Moderately similar to S12207_hypothetical protein 1 (Mus musculus)	1.0	-1.4	1.0	-1.2	-2.0	-1.0	1.1	1.0	-1.2	-1.4	-1.1	-1.2
A467288 Mouse mRNA for T1-227	-1.5	-1.3	-1.0	-1.1	-2.1	1.2734	-1.1	-1.1	-1.0	-1.3	-1.1	-1.2
A419404 ESTs	-1.1	-1.7	-1.1	-1.0	-2.1	-1.4579	-1.37782	1.2	1.0	-1.1	1.1	1.0
W15903 Omeprazole, azox, heavy chain 11	1.3	-1.3	-1.1	-2.5	-2.1	-1.8	-1.1	1.0	-1.1	-1.2	-1.2	-1.1
A4450917 RIKEN cDNA 181005K14 gene	-1.1	-1.0	-1.0	-1.4	-2.1	-1.1	-1.4	-1.1	-1.1	-1.1	1.1	-1.1
A486008 ESTs, Highly similar to GUANINE NUCLEOTIDE-EXCHANGE PROTEIN 13 (Mus musculus)	-1.2	-1.2	-1.1	1.0	-2.1	-2.3728	1.1	-1.1	-1.0	-1.1	-1.1	-1.2
A4914844 Public domain EST	1.3	-1.5	1.0	-1.2	-2.1	1.0	1.0	1.2	-1.1	-1.3	1.1	-1.1
A492688 protein phosphatase, EF hand calcium-binding domain 2	1.1	-1.5	-1.1	-1.1	-2.1	1.1	1.02202	1.2	-1.1	-1.3	1.1	-1.1
A490737 test shock protein cognate 70	1.0	-1.1	-1.0	-2.1	-2.1	-1.5	-1.1	1.3	1.5	1.3	1.0	1.2
A450446 ESTs	-1.8	-1.1	-1.7	-1.2	-2.1	-2.0061	-1.9	-1.2	1.0	-1.1	-1.0	-1.1
A4518915 RIKEN cDNA 111001M06 gene	1.2	-1.3	1.1	1.3	-2.1	-1.0	1.6	1.3	1.1	-1.1	1.2	-1.0
A450282, related cdc14 homolog (Crotaphaga)	-1.0	-1.3	-1.0	1.0	-2.1	1.0	1.0	1.3	-1.1	-1.3	1.2	-1.1
A460713 Mus musculus 10 day old male pancreas cDNA_RIKEN f11-length, enriched library, clone:181006A17, full insert sequence	1.1	1.5	-1.2	-1.5	-2.1	-1.5	-1.7	1.4	-1.0	-1.1	1.5	1.4
A4152940 Immunoglobulin kappa chain variable 2B (V2B)	1.3	-1.0	-1.5	-1.0	-2.1	-3.1	-2.2	-1.3	-1.3	-1.6	-1.1	-2.5
A460118 ESTs	-1.6	-1.025164	1.3	-1.1	-2.1	1.37098	1.3	-1.2	-1.1	1.1	-1.0	1.3
A4290095 ESTs	-1.1	-1.3	1.0	-2.1	-2.1	-1.1	-1.2	1.2	-1.0	-1.2	1.1	-1.1
A4444578 test shock protein, 60 kDa	1.1	-1.1	1.4	-1.8	-2.2	-1.2	1.0	1.1	1.0	-1.1	-1.1	-1.2
A461754 ESTs	1.0	-1.3	-1.0	1.1	-2.2	1.3	-1.1	1.3	1.0	-1.1	1.2	-1.1
A4019837 myosin beta 3	1.1	1.4	-1.1	-1.5	-2.2	-2.16452	1.21089	1.5	-1.1	1.1	1.1	1.4
A468404 typosomerase (DNA II) beta	1.1	-1.2	-1.2	-2.2	-2.2	1.0	-1.2	-1.5	-1.2	-1.5	-1.3	-1.2
A460295 immunoglobulin joining chain	1.2	-1.5	-1.4	-1.7	-2.2	-2.4	-1.9	-1.1	1.3	1.5	1.4	-1.3
A4200308 ESTs	-1.5	-1.3	-1.5	-1.0	-2.2	1.06091	1.1	-1.2	-1.3	-1.3	1.1	-1.1

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A040294 ESTs, Weakly similar to 529170, laminin, VII, mouse [Mus musculus]	-4.1	-1.1	-1.2	-2.2	-1.9222+	1.5	-1.1	1.3	1.5	-1.1	-1.1
W56956 hemoglobin X, alpha-like, embryonic chain in this complex	1.1	-1.6	-1.3	-1.2	-2.2	1.1222+	-2.1	-2.0	1.0	-1.2	-4.0
A028278 ESTs	-1.3	-1.5	-1.3	-2.2	-1.91004+	-1.4	-1.0	-1.2	-1.4	1.2	-1.0
A040378 ESTs, Moderately similar to 514294, hypothetical protein, mouse [Mus musculus]	1.0	-1.3	-1.0	-1.2	-2.2	-1.1	1.2	1.1	-1.3	1.0	-1.2
AA116285 integrin, alpha 4	1.2	-2.2	-1.3	1.1	-2.2	1.1	-1.0	1.3	-1.9	-1.4	-1.2
AA138554 ESTs, Weakly similar to tyrosinophosphatase 1 [Mus musculus]	-1.4	-1.6	-1.1	-1.0	-2.3	-2.1	1.1	-1.7	-1.0	1.4	-1.1
AA117298 Parvulin, cell enriched expression	1.3	-1.2	1.1	-2.3	-1.28142+	-1.6	1.2	-1.0	-1.8	1.0	-1.2
A052114 methionine co-factor synthesis 2	1.1	-1.7	-1.0	1.2	-2.3	1.2	1.1	1.3	1.0	-1.3	1.3
AA439317 ESTs	-1.2	-1.7	1.1	-1.0	-2.3	1.1	-1.1	-1.1	-1.5	-1.4	1.1
AA100592 Eukon, epimerase/hydrolase, lysine, lysine, regulated, protein, 75MD	-1.4	1.0	1.2	-1.4	-2.3	1.05592+	-1.53074+	-1.4	1.0	-1.2	-1.2
AA44865 ESTs	1.1	1.7	-2.4	-2.2	-2.4	-1.6	1.0	-1.3	1.2	1.1	-1.1
AA44865 ESTs	1.0	-1.1377+	1.02881+	1.2	-2.4	-1.0147+	-1.3	1.03478+	1.2	1.3	1.1
AA176095 ESTs	-1.6	-1.3	-1.2	-1.3	-2.4	-1.2	-1.2	-1.2	-1.4	-1.3	-1.4
AA212405 cinnamylolase, nudage	-1.2	-1.6	-1.2	-1.0	-2.5	-2.6	1.1	-1.4	-1.2	1.1	-1.1
AA272065 ESTs	1.1	-1.2	1.2	-2.1	-2.5	1.2	-1.2	-1.6	-1.2	-1.4	-1.3
AA44865 ESTs	-1.3	1.1	1.0	-1.3	-2.5	-1.1	-1.4	-1.2	-1.2	-1.4	-1.1
A057143 ESTs	-1.0	-1.1	1.1	-1.3	-2.5	-3.6	1.2	-1.1	-1.2	-1.1	-1.0
A0459794 AXV, nuclear, tyrosine kinase	-1.3	1.0	1.1	1.0	-2.6	1.01592+	-1.6	-1.1	1.1	-1.1	-1.1
A030651 retinoic acid induced 1	-4.5	1.0	-1.3	-1.2	-2.6	1.01684+	-1.1	-1.3	-1.3	-1.1	-1.2
AA116984 nuclear receptor coactivator 4	1.4	-1.3	1.4	-1.7	-2.7	-1.0	1.1	1.1	1.2	1.3	-1.1
AA448674 kallidin, 6	1.3	1.5	-1.2	-1.3	-2.7	-2.3	-1.2	-2.8	-1.6	1.1	1.0
A052627 rhodanin protein, L28	1.2	1.1	1.3	-1.8	-2.7	-1.2	1.2	-1.2	1.1	-1.1	-1.2
AA521093 Public domain EST	-1.6	-1.3	-1.6	-1.5	-2.7	-1.5	-1.2	-1.0	-1.5	-1.1	-1.3
AA310805 Public domain EST	1.4	-1.5	1.2	-2.1	-2.7	-1.7	-1.1	1.1	1.3	1.1	1.2
AA242980 cytochrome P450, 1A2, aromatic compound inducible	1.3	-1.5	1.4	-1.1	-2.8	-1.33655+	-1.37534+	-2.4	1.0	1.1	1.2
A059392 G, protein-coupled receptor, family C, group 5, member B	-1.3	-1.7	-1.4	-2.1	-2.9	-1.3	-1.6	-1.1	-1.3	-1.1	-1.0
AA430001 alkaline phosphatase 5	1.14657+	-1.15714+	1.35347+	-1.05793+	2.9	1.52048+	1.07417+	-1.01637+	-1.07118+	-1.19807+	1.08192+
AA100600 glutathione S-transferase, alpha 4	1.1	1.0	1.6	-2.4	-3.0	1.3	1.2	1.0	1.3	1.3	-1.1
A026739 ESTs, Weakly similar to ACRC, HUMAN ACROSIN, PRECU, RSD, IT, ligand	1.3	-1.6	-1.3	-1.1	-3.2	1.0	-1.0	-1.1	-1.3	-1.3	-1.3
A076007 RIKEN cDNA, 221047F13, gene	1.01657+	-1.36629+	1.0	1.2	3.5	-1.03402+	-1.06819+	1.2	-1.0	1.1	1.3
A014443 5-phosphoadenosine 5-phosphothiolate synthase 2	1.2	-1.2	1.5	1.2	3.7	-1.4	-1.3	1.4	1.5	1.3	1.2
AA593438 cathepsin, E	-1.0	-1.5	1.0	-1.6	-4.1	-1.6	-1.5	-1.1	-1.1	-1.3	1.1
A065544 small protein-rich protein 2A	-1.0	-1.1	-1.4	-1.3	-5.5	-3.9	1.0	-1.2	-1.2	-1.1	-1.5

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A327450 phospholipase A2_group IB_pancreas	1.3	18	1.1	-18	-3.7	1.01624	-23	-1.6	-1.4	-1.1	-1.0
A674409 pancreatic lipase related protein 1	2.0	17	-1.4	-17	-5.9	-10	1.2	1.0	-1.1	-1.1	-1.3
A447618 ctn-ductin	1.7	19	-1.1	-16	-6.1	-5.0	1.5	-1.2	-1.3	-1.2	1.5
W12895_arsenite A10	-1.1	-1.4	-1.3	-21	-6.1	1.61614	-1.8	-2.1	-1.0	-1.1	-1.4
A4107101 prosaba stem cell antigen	1.6	-1.7	-1.1	-23	-6.5	-1.03587	-1.3	-1.1	1.1	-1.0	-1.9
A876967 carboxyl ester lipase	1.5	15	-1.4	-23	-4.9	-1.9	-1.3	-1.4	-1.1	1.1	-2.0
A4982264 RIKEN cDNA 271001C04 gene	2.3	15	-1.3	-20	-9.5	-1.3	1.6	-1.5	-2.0	-1.4	-1.1
A457793 rat regenerating liver-derived mouse homolog 1	2.6	14	-1.3	-3.9	-11.8	-2.2	1.0	-1.4	-2.7	-1.2	-1.2
A675111 RIKEN cDNA 181007X24 gene	1.4	13	-1.0	-21	-14.0	-1.5	1.0	-1.4	-2.2	-1.2	-2.0
A451862 RIKEN cDNA 091001A18 gene	1.6	13	-1.1	-25	-14.7	-2.8	1.2	-1.3	-2.4	-1.3	-1.3
A386604 brycin 4	1.7	13	1.1	-18	-15.9	-2.6	1.8	-1.5	-2.5	-1.1	-1.2
A476209 fibronectase 1, pancreatic	1.7	13	-1.2	-5.8	-16.6	-3.3	1.7	-1.9	-4.1	-1.1	-1.1
A675924 elastase 2	2.5	14	-1.2	-27	-21.7	-2.2	1.7	-1.9	-4.0	-1.4	-1.4
A477703 Mus_musculus_10 day old male pancreas cDNA_RIKEN f	1.9	-1.1	-1.2	-27	-25.5	-5.2	2.1	-1.8	-2.9	1.2	-1.1
ul-triethyl enriched library, clone B1006A17, full insert sequence	3.1	1.1	-1.2	-2.8	-32.0	-4.0	2.5	-1.2	-4.4	-1.1	-1.2
A482184 amylase 2, pancreatic	-2.2	-1.3	1.2	1.5	-53.5	-4.1	1.0	-1.2	-1.1	-1.2	1.4
A386297 calthidin-ORF	-1.1	1.8	-1.2	-2.0	-32.1	-1.8077	-1.4	1.0	-1.4	-1.9	-1.0
A864332 rateli factor 2 (esamoylase protein 1)											

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stomach	spl	panc	liv	stom	int	col	brain	lung	blad	kidn	p/lut	mam
	PK- 48, BODiver	PK- 48, BODiver	PK- 48, BODiver	PK- 48, BODiver	PK- 48, BODiver	PK- 48, BODiver	PK- 48, BODiver	PK- 48, BODiver	PK- 48, BODiver	PK- 48, BODiver	PK- 48, BODiver	PK- 48, BODiver
Description												
A1549024 RIKEN cDNA, 1619414E0, gird	1.6	1.4	-1.3	3.6	1.9	-1.01548+-	1.1	2.2	2.1	1.6	2.5	2.3
AAB17Y12 ESTs	1.4	1.4	-1.2	3.3	1.7	-1.01871+-	1.3	1.6	1.7	1.3	1.8	1.9
A1804567 ESTs	1.2	1.3	-1.1	3.5	1.5	-1.02494+-	1.2	1.5	1.6	1.3	1.5	1.6
A5444433 dihydrocarate, dihydrogenase	1.2	1.5	1.0	3.2	1.7	1.24371+-	1.4	1.6	1.7	1.4	2.0	1.7
A4468350 cholone, kinase	1.7	1.9	-1.4	3.1	2.0	1.31548+-	1.3	2.3	2.0	1.6	2.2	2.1
A431982 EST	1.5	1.7	1.0	2.9	1.4283+	-1.00684+-	1.8	2.33182+	2.06474+	1.6	2.5	2.0
A1653602 RIKEN cDNA, 1700049D1, gene	1.35465+	1.07634+	1.02965+	2.9	1.17207+	-1.35039+-	1.75338+	1.1648+	1.29228+	1.4	1.2	1.13038+
A4607597 Public, domain EST	1.4	1.7	-1.5	2.9	1.6	-1.07432+-	1.5	1.7	1.8	1.5	1.7	1.7
A1649854 programmed, cell, death, 10	1.24627+	2.02725+	-1.00384+	2.6	1.6	1.10261+-	2.810244+	1.76339+	1.600344+	1.3	1.6	1.6
A1561920 RABP1, associated, Eps domain, containing, protein	1.4	1.7	-1.1	2.6	1.5	-4.1	1.2	1.8	1.9	1.7	2.0	1.7
A1035904 ESTs, Weakly, similar, to, X-LINKED, LYMPHOCYTE, REGULATED, PROTEIN, PM, [M, nucleus]	1.34109+	1.0	1.1	2.6	1.7	-1.23681+-	1.1	1.6	1.4	1.1	1.5	1.6
A1581381 ESTs, Weakly, similar, to, FVL, MOUSE, FRIEND, VIRUS, SUSCEPTIBILITY, PROTEIN, 1, [M, nucleus]	1.2	1.71031+	-1.05799+	2.7	1.7	1.64433+-	2.6	1.77633+	1.6	1.5	1.6	1.6
A2264406 nuclear, factor, /B	1.4	1.1	-1.3	2.7	1.6	-1.28971+-	1.4	1.4	1.2	1.3	1.7	1.2
A1587592 RIKEN cDNA, 0710001D01, gene	1.4	1.3	-1.3	2.7	1.5	-1.26826+-	1.4	1.5	1.7	1.3	1.6	1.5
A1116478 [M, nucleus, cDNA, (SC10), for, Ipa, 100, heavy, chain, -1.3	-1.3	1.0	-1.6	2.7	-2.0	-2.4	-1.1	-1.4	1.5	2.0	1.1	1.6
A1158726 [protein, tyrosine, phosphatase, ectopic, 5/12, -1.02687+	1.02687+	1.1	-1.25592+	2.6	1.1	1.01781+-	1.2	1.3	1.0	1.1	1.1	1.3
A100394 ESTs, Moderately, similar, to, No, immediate, early, induced, protein, [L, spleen]	1.1	1.0	-1.3	2.6	-1.1	-1.23021+-	2.3	1.0	-1.2	1.2	-1.2	-1.0
A4723916 ESTs	1.0	1.2	-1.1	2.6	1.5	-1.12264+-	1.7	1.3	1.4	1.3	1.6	1.5
A6534076 ESTs	1.1	1.5	-1.5	2.6	1.7	1.17811+-	2.3	1.33689+	1.7	1.4	1.6	2.7
A1162022 ESTs	1.3	1.5	-1.1	2.6	1.7	1.36792+-	1.3	1.7	1.8	1.2	1.7	1.6
A1073222 ESTs	1.3	1.6	-1.4	2.6	2.0	1.27077+-	1.1	1.3	1.9	1.2	1.6	1.9

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A168240F DNA polymerase epsilon	1.1	1.2	-1.4	2.5	1.6	-1.2103+-	-1.0	1.6	1.4	1.3	1.3	1.3
A168167F ESTs	1.2	1.3	-1.3	2.5	1.6	1.00205+-	1.6	1.3	1.5	1.5	1.3	1.6
A162464F Public domain EST	-1.00414+-	1.6	-1.1	2.5	1.1	1.06724+-	1.4	1.3	1.5	1.1	1.3	1.4
A44180F ESTs	1.1	1.7	1.0657+-	2.5	1.6959+-	-1.0806+-	2.5	1.5	1.2	1.6	2.1	2.1
A41167S RIKEN cDNA 2810018C03 gene	1.1	-1.8	-1.5	2.4	1.3	1.22789+-	1.5	1.5	1.5	1.3	1.5	1.5
A427048F ESTs	1.7	1.3	-1.1	2.4	1.5	1.2463+-	1.2	1.6	1.7	1.4	1.5	1.9
A423587F ESTs	1.1	1.3	-1.3	2.4	1.5	-1.10189+-	1.2	1.6	1.6	1.2	1.5	1.7
A462000 RIKEN cDNA 2416124L17 gene	1.5	1.5	1.1	2.4	1.36143+-	-1.3	1.6	1.7742+-	1.7	1.4	2.0	1.8
A161844F ESTs, Weakly similar to C237S acyl-CoA C-acyltransferase [Haploma]	1.2	1.1	-1.4	2.4	1.3	1.05498+-	1.4	1.6	1.7	1.7	1.7	1.6
A470284F binding protein kinase 8	1.1	1.0	-1.3	2.4	1.3	1.3	1.5	1.4	1.5	1.2	1.2	1.3
A411279 RIKEN cDNA C230003J06 gene	1.6	1.8	-1.0	2.4	1.2	-1.3	1.3	2.0	1.0	1.5	1.7	1.7
A4607693F zinc finger protein 101	1.23774+-	1.9	-1.36204+-	2.4	1.6	1.1264+-	1.65168+	1.432+	1.5	1.2	1.4	1.7
A161732F RIKEN cDNA 261030115 gene	1.3	2.07861+-	1.1	2.4	1.5	1.2409+-	2.9	1.4	1.5	1.6	1.5	1.0
A463845F growth factor, wnt-3 (cysteine) like (segment of liver regeneration)	1.4	1.6	-1.4	2.4	1.6	1.3548+-	1.5	1.4	1.5	1.3	1.5	1.4
A163526F ESTs	1.22088+-	1.2	-1.26881+-	2.4	1.46785+-	-1.26469+-	1.45708+	1.46404+-	1.53133+-	1.7	1.7476+-	1.32952+-
A162315F ESTs	1.5	1.5	-1.0	2.4	1.6	-1.39002+-	1.4	2.3	2.1	1.7	2.2895+-	1.6
A165470F ESTs	1.2	1.2	-1.2	2.4	1.5	-1.0	1.4	1.5	1.3	1.4	1.3	1.4
A148449 RIKEN cDNA 19851516C6 gene	1.3	1.7	-1.1	2.4	1.4	1.0667+-	1.4	1.5	1.6	1.4	1.9	1.6
A1628005F Public domain EST	1.1	1.5	-1.2	2.3	1.6	-1.12798+-	1.4	1.6	1.6	1.3	1.5	1.7
A165097F ESTs	-1.0	1.3	-1.1	2.3	1.3	-1.1035+-	1.5	1.6	1.4	1.2	1.5	1.5
A1663769F struct_L (client_testing_type information, regulation_2, homolog 1) (S. cerevisiae)	1.1	1.3	-1.2	2.4	1.5	-1.2284+-	1.2	1.4	1.1	1.3	1.3	1.3
A164064F ESTs, identical to F500 ALMAN_E1A-ASSOCIATED PROTEIN P203 (Hspp26)	1.0	1.1	-1.3	2.3	1.3	1.1593+-	-1.1	1.4	1.7	1.4	1.6	1.8
A165020F SECT1, alpha subunit 2 (S. cerevisiae)	1.3	1.6	1.1	2.3	1.6	1.2843+-	1.2	1.5	1.6	1.5	1.4	1.7
A1614543F displacins homolog 3 (Drosophila)	1.2	1.6	-1.3	2.3	1.7	1.0107+-	1.8	1.5	1.3	1.2	1.3	1.4
A4231009F acodin	-1.8	1.3	1.1	2.3	1.7	1.56	1.0	2.0	-1.3	1.2	-1.7	1.0
A16591029F ESTs	1.20192+-	1.40656+-	1.03838+-	2.3	1.43296+-	-1.18503+-	2.2592+	1.35448+-	1.30148+	1.3	1.5	1.1

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AA52219 ESTs	1.2087+	1.076+	-1.18583+	2.3	1.3	-1.36749+-	2.1407+-	1.53406+	2.1	1.8	1.85635+	1.8719+
AA517891 ESTs	1.3	1.6	-1.2	2.3	1.321467	-1.2	1.6	1.3	1.7	1.5	1.6	1.5
AA517331 VASP family_1	1.1	1.0	-1.6	2.3	1.4	-1.40453+-	1.5	1.1	1.4	1.2	1.2	1.3
AA543850 RIKEN_cDNA_2900079C15_gene	1.1	1.4	-1.2	2.3	1.2	-1.06831+-	-1.1	1.5	1.3	1.2	1.5	1.6
AA417352 low density lipoprotein receptor-related protein_2	1.1	1.4	-1.1	2.3	1.4	-1.17936+-	1.53061+	1.1	1.5	1.4	1.0	1.7
AA417984 RIKEN_cDNA_C00002017_gene	1.22138+	1.50183+	-1.02182+	2.2	1.37779+	-1.21258+-	2.0	1.50959+	1.3067+	1.6061+	2.24475+	1.7053+
AA253337 deoxycholate diase	1.1	1.1	-1.2	2.2	1.4	-1.04367+-	1.1	1.4	1.7	1.3	1.2	1.5
AA559881 Mus musculus brain cDNA clone M106-160	1.0	1.1	-1.2	2.2	1.5	-1.12938+-	1.0	1.3	1.1	1.2	1.3	1.1
AA267871 ESTs, Weakly similar to 317717_1/any/mus_musculus_	1.4	1.3	-1.1	2.2	1.6	1.11463+-	1.5	1.5	1.1	1.4	1.5	1.4
AA554_R1025358381	1.2	1.4	-1.22779+	2.2	1.4	-1.1	1.1	1.5	1.4	1.2	1.3	1.4
AA49955 ESTs	1.35491+	1.35116+	1.04833+	2.2	1.08107+	1.52763+-	1.07014+	1.5	1.071	1.2	1.5	2.03047+
AA52572 ESTs, Highly similar to 23911 (R. norvegicus)	1.3	1.2	-1.2	2.2	1.2	-1.10963+-	1.3	1.2	1.3	-1.1	1.2	1.3
AA210502 Public domain EST	1.1	1.7	-1.2	2.2	1.5	1.05245+-	1.17892+	1.6	1.5	1.5	1.4	1.7
AA509884 RIKEN_cDNA_241074K12_gene	-1.0	1.1	-1.1684+	2.2	1.1	-1.18468+-	1.7	1.0	1.1	1.1	1.1	1.1
AA577955 ESTs	-1.0	1.1	-1.1	2.2	1.4	1.2339+-	1.33244+	1.2	1.4	-1.1	1.3	1.5
AA400552 Public domain EST	1.3444+	1.5	-1.2	2.2	1.4	1.06501+-	1.8	1.5	1.3	1.3	1.5	1.6333+
AA511955 RIKEN_cDNA_333014E02_nore	1.0	1.3	1.4	2.2	1.4	1.87213+-	-1.2	1.2	1.1	1.3	1.2	1.6
AA429452 ESTs	1.4959+	1.3503+	-1.08199+	2.2	1.54602+	1.02451+-	1.9	1.31404+	1.39275+	1.2	1.8	1.40132+
AA210270 ESTs, Weakly similar to 117254_1/hypothetical_protein_DN2565	1.1	1.3	-1.2	2.2	1.3	-1.1	1.4	1.4	1.4	1.2	1.67827+	1.4
AA412812 ESTs	1.2	1.5	-1.4	2.2	1.5	-1.07079+-	1.9	1.6	1.7	1.2	1.5	1.6
AA209824 hydroxyacid oxidase (glyoxylate oxidase)_3	1.3	1.3	-1.2	2.2	1.32102+	-1.2	1.4	1.3	1.1	1.3	1.5	1.5
AA209824 hydroxyacid oxidase (glyoxylate oxidase)_25	1.0	-1.0	-1.0	2.2	1.5	1.57768+-	1.4	-1.0	1.5	1.2	1.3	1.7
AA709579 ESTs	1.1	1.1	-1.14548+	2.2	1.5	1.02803+-	1.5	1.33339+	1.4	1.4	1.1	1.1
AA411551 RIKEN_cDNA_483343K12_gene	1.27918+	1.1	-1.0	2.2	1.9	-1.14544+-	1.9	1.6	1.3	-1.1	1.4	1.3
AA000370 RIKEN_cDNA_483343K12_gene	1.3	1.1	-1.5	2.2	1.9	1.17842+	1.4	1.5	1.0	1.3	1.3	1.3
AA411551 RIKEN_cDNA_483343K12_gene	1.3	1.6	-1.0	2.2	1.7	1.55578+-	1.3	1.8	2.0	1.5	1.8	1.8
AA15231 ESTs, Moderately similar to unnamed protein product_14 sample	1.1	1.4	-1.1	2.2	1.0	1.11879+-	-1.5	1+	1.0	-1.1	1.3	1.4
AA15231 ESTs, Moderately similar to unnamed protein product_14 sample	1.2	1.2	-1.1503+	2.2	1.4	1.15298+-	1.7	1.4	1.4	1.2	1.2	1.2
AA15232 ribosomal protein S9	-1.0	1.0	-1.1	2.2	1.4	1.45741+-	1.14599+	1.4	1.5	1.2	1.4	1.3
AA210500 Mus musculus. Similar to RIKEN_cDNA_150004N16_gene_0	1.2	1.5	1.0	2.2	1.2	1.20592+-	1.9	1.6	1.6	1.4	2.2	1.7
one MGC-12059 cDNA, complete cds	1.2	1.6	-1.0	2.2	1.3	1.17169+-	1.4	1.62347+	1.5	1.4	1.5	1.3
AA037649 transition protein_1	1.1	1.2	-1.2	2.1	1.4	-1.3	-1.4	1.5	1.2	1.2	2.3	1.2
AA17167 c16a6a.1 lymphocyte-associated protein_2_alpha	1.4	-1.8	-1.3	2.2	1.4	1.1	-1.8	-1.1	1.5	-1.4	-1.5	1.8

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AA183586	ESTs, Moderately similar to T00076 hypothetical protein_KIAA0461 [Rhesus]	1.1	-2.8	1.0	2.1	1.5	1.06058+-	1.3	1.4	1.2	1.6	1.3	1.3
AA170379	neurodin	-1.06003+	1.2	1.3	2.1	1.4	-1.63798+-	-1.1	1.1	1.2	-1.1	1.3	1.4
AA183731	ESTs	1.2	1.5	-1.4	2.1	1.3	-1.00765+-	1.5	1.5	1.4	1.4	1.3	1.0
AA710200	ESTs	1.2	1.4	1.01548+	2.1	1.2	-1.28971+-	1.0	1.2	1.2	1.1	1.1	1.1
AA184900	ESTs	1.2	1.0	-1.5	2.1	1.1	-1.07437+-	1.4	1.4	1.2	1.3	1.4	1.4
AA183201	Mus musculus TOR3 mRNA, complete cds	1.3	1.9	1.1	2.1	1.5	1.20083+-	1.2	1.4	1.5	1.5	1.4	1.4
AA145967	Riken cDNA 432401C08, gene	1.3	1.2	-2.0	2.1	-1.0	1.1	1.3	-1.2	1.5	1.4	1.6	1.9
AA183769	synanth binding protein 1	-1.2	1.2	1.3	2.1	1.4	1.6644+-	1.3	-1.2	-4.3	-1.1	-1.0	1.1
AA183578	wnt gene homolog (Drosophila)	-1.1	1.1	1.7931+	2.1	1.4	2.1	-1.2	-1.3	1.1	1.0	-1.2	-1.0
AA156461	Riken cDNA 24-0044K02, gene	1.2	1.5	-1.4	2.1	1.7	1.52803+-	1.3	1.4	1.3	1.2	1.6	1.4
AA23742	Riken cDNA 1110056A2, gene	1.1	-1.0	-1.1	2.1	1.3	1.06169+-	1.2	1.3	1.2	1.2	1.3	1.5
AA18414	cDNA, segment, Clontech, Clontech	1.1	1.3	-1.2	2.1	1.4	1.17655+-	1.1	1.5	1.3	1.2	1.2	1.3
AA18378	Mus musculus, clone MGC-7945, mRNA, complete cds	1.3	1.3	1.0	2.1	1.1	1.45689+-	1.5	1.5	1.5	1.2	1.5	1.4
AA235051	myosin heavy polypeptide 3, skeletal muscle, embryonic	1.4	1.5	-1.2	2.1	1.3	1.19039+-	1.4	1.77337+	1.5	1.4	1.5	1.6
AA107400	core_1_UDP-glucosyl-N-acetylglucosaminyltransferase_1,3-2-6-beta-transferase	1.4	1.6	-1.3	2.1	1.5	1.14933+-	1.5	1.7	1.5	1.3	1.6	1.5
AA450351	BCL2/adenovirus E1B 19 kDa-interacting protein 1, NP2	1.2	1.2	1.1	2.1	1.4	1.70102+-	1.3	1.1	1.2	1.1	1.1	1.0
AA633776	matrix metalloproteinase 12	1.26422+	1.5439+	-1.11429+	2.1	1.4	1.01189+-	1.04811+	1.28335+	1.4481+	1.4	1.2	1.48751+
AA110551	glucosylidyl transferase 2	1.1	-1.1	-1.1	2.1	1.7	1.1	-1.4	1.2	1.8	-1.0	1.2	1.2
AA183106	Riken cDNA 482431P02, gene	1.4	1.5	-1.2	2.1	1.4	-1.0	1.4	1.6	1.6	1.4	1.5	1.6
AA55056	seracyl-CoA desaturase 2	1.4	1.2	-1.3	2.1	1.4	-1.5	2.0	1.5	1.5	1.2	1.4	1.3
AA65510	myel cell protease 2	1.12172+	1.2916+	1.09121+	2.1	1.62333+	1.02511+-	1.21528+	1.21528+	1.0051+	-1.07124+	1.2851+	-1.1
AA112021	Riken cDNA 4621514120, gene	1.4	1.6	1.0	2.1	1.4	-1.23077+-	1.5	1.7	2	1.4	1.6	1.5
AA52048	ESTs	-1.04637+	1.2062+	-1.0	2.1	1.39436+	1.16278+-	-1.03946+	1.19454+	1.2	-1.0	1.3	-1.0
AA285101	Riken cDNA 180021C18, gene	1.4	1.2	-1.1	2.1	1.1	1.03833+-	-1.3	1.3	1.3	1.1	1.3	1.4
AA556867	ESTs, Weakly similar to Inv Mmusculal	1.2	1.4	-1.35747+	2.1	1.5	1.19833+-	1.4	1.3	1.2	1.0	1.3	1.1
AA251697	kinase suppressor of ras	1.1	1.2	-1.4	2.1	1.4	1.1794+-	1.2	1.2	1.4	1.2	1.3	1.4
AA254235	complement receptor 2	1.1	1.5	-1.1	2.1	1.4	-1.02477+-	1.5	1.4	1.2	1.1	1.4	1.3
AA150452	Riken cDNA 843043L24, gene	1.2	1.5	-1.2	2.1	1.5	1.20033+-	1.4	1.3	1.5	1.1	1.4	1.4
AA584430	galactose-1-epimerase (ecoli transfrase)	1.3	1.5	-1.0	2.1	1.4	-1.08755+-	1.4	1.6	1.4	1.2	1.4	1.1
AA073720	ESTs	1.2	1.5	-1.1	2.1	1.2	1.0728+-	1.5	1.5	1.5	1.1	1.5	1.3
AA287824	Public domain EST	1.3	1.6	-1.1	2.1	1.32119+	1.13095+-	1.3	1.1	1.5	1.3	1.5	1.5
AA657043	Riken cDNA 240007507, gene	1.1	1.4	-1.1	2.1	1.5	1.10333+-	1.3	1.3	1.4	1.4	1.3	1.3
AA273401	Public domain EST	1.5	1.3	-1.0	2.1	1.40023+	-1.0	1.3	1.5	1.5	1.4	1.5	1.6

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AA65928	RIKEN cDNA A330103N21 gene	1.3	1.2	-1.2	1.4	1.1	1.3	1.4	1.3	1.4	1.3	1.4	1.3
AA54720	ESTs, Weakly similar to JH0494	1.2	1.4	1.1	1.2	-1.1432+	1.1	1.4	1.5	1.3	1.4	1.3	1.3
AA61974	MM domain, bcl-2, protein 5	1.3	1.4	-1.1	2.0	1.5	1.0	1.1	1.7	2.0	1.3	1.6	1.5
AA474374	RIKEN cDNA 572040C10 gene	1.3	1.5	1.0	2.1	1.3	-1.07742+	1.5	1.4	1.3	1.4	1.5	1.6
AA45048	Mus, musculus, Similar to hypothetcal protein, clone JMC5756	1.4	1.3	-1.2	1.4	1.02813+	1.3	1.3	1.2	1.5	1.3	1.3	1.3
AA79227	Procollagen, type V, alpha 1	1.2	1.0	-1.16089+	1.5	1.4	-1.4	1.0	1.2	1.1	-1.1	-1.3	1.4
AA10837	perid, homolog 3, (Drosophila)	1.2	1.1	-1.1	2.0	1.2	1.11211+	1.3	1.3	1.1	1.4	1.4	1.4
AA46199	RIKEN cDNA 241005N02 gene	1.3	1.5	-1.20814+	1.4	1.0388+	1.2	1.2822+	1.2	1.7427+	1.2	1.2	1.2
AA20475	ESTs	1.2	1.1	-1.7	1.4	1.43838+	1.3	1.5	1.4	1.2	1.3	1.3	1.3
AA53819	ras, junction, membrane channel, protein, beta 3	1.2	1.5	-1.1	2.0	1.2	-1.3763+	1.5	1.4	1.3	1.4756+	1.4	1.3
AA32924	Mus, musculus, Similar to proprotein regulated by nitric oxide, proteinase, clone JMC 1178, (rRNA, complete cds)	1.3	1.4	-1.1	2.0	1.4	-1.2	1.3	1.5	1.2	1.5	1.5	1.5
AA55259	Public domain EST	1.1	1.2	-1.1	2.0	1.4	1.40334+	1.4	1.4	1.1	1.3	1.5	1.5
AA47124	DNA segment, Chr 2, ERATO D01 435, expressed	1.2	1.2	-1.1	2.0	1.4	-1.0	1.5	1.4	1.3	1.2	1.2	1.2
AA69546	ESTs, Weakly similar to SFRE HUMAN SPLICING FACTOR, (HUMAN SPICE-PCR1.1) (partial)	1.3	1.2	1.2	2.0	1.1	-1.4088+	1.5	1.5	1.4059+	1.3	1.7	1.5
AA89189	clathrin, related cytopl, related sequence 10	-1.0	-1.1	-1.7	2.0	2.3	1.5	1.2	1.2	1.1	1.2	1.2	1.2
AA15597	ESTs	1.3	1.5	-1.1	2.0	1.2	-1.2	1.4	1.6	1.3	1.2	1.5	1.5
AA10807	RIKEN cDNA 280007D14 gene	1.4	1.1	1.1	2.0	1.2	-1.2	1.4	1.6922+	2.0	1.2	1.7	1.6
AA15597	ESTs	1.2	1.4	-1.3	2.0	1.5	-1.5	2.0	1.4	1.4	1.2	1.5	1.6
AA51688	ESTs	1.2	1.4	-1.3	2.0	1.5	-1.5	2.0	1.4	1.4	1.2	1.5	1.6
AA15307	ESTs	1.2	1.2	-1.3	2.0	1.5	-1.0288+	1.2	1.5	1.3	1.0	1.3	1.3
AA204049	Public domain EST	1.4	1.4	1.1	2.0	1.3	-1.2	1.1	1.6	1.3	1.3	1.3	1.3
AA212102	ESTs	-1.1	1.3	-1.1	2.0	1.2	1.16314+	1.7	1.1	1.9	1.1	1.1	1.3
AA55921	ESTs	1.3	1.3	-1.0	2.1	1.1	-1.0	1.8	1.3	1.1	1.3	1.2	1.2
AA470247	nitrogen regulated protein, protein 3	-1.0	1.0	-1.3	2.0	1.1	-1.0	-1.8	1.7	1.1	1.0	-1.8	1.4
AA48544	RIKEN cDNA 111005S105 gene	1.3	1.3	-1.1	2.0	1.3	1.0	1.4	1.5	1.4	1.3	1.5	1.4
AA48544	RIKEN cDNA 111005S105 gene	-1.1	1.3	1.0	2.0	1.3	-1.0634+	1.8	1.0	1.2	1.3	-1.0	1.2
AA48544	RIKEN cDNA 111005S105 gene	-1.1	1.3	1.0	2.0	1.3	-1.0634+	1.8	1.0	1.2	1.3	-1.0	1.2
AA56075	ESTs	-1.0	1.26978+	-1.3	2.0	1.1	1.12054+	1.1	1.3	1.1	1.2	1.2	1.3
AA49727	interactin (SH3 domain protein 1A)	-1.8	1.0	1.1	2.0	1.5	2.0772+	-1.0	-1.8	-1.5	-1.2	-2.1	-1.2
AA717000	ESTs	1.0	1.2	-1.1	2.0	1.6	1.8571+	-1.2	1.2	1.2	1.1	1.2	1.2
AA244613	subunit 2	1.4	1.1	-1.5	2.0	1.6	1.16191+	1.3	1.4	1.2	1.3	1.5	1.7
AA238048	ESTs	1.2	1.3	1.1	2.0	1.3	-1.08024+	1.5	1.5	1.4	1.2	1.5	1.5
AA46460	RIKEN cDNA 071001E13 gene	1.1	1.1	1.0	2.0	1.4	-1.0888+	1.2	1.0953+	1.4	1.2	1.4	1.4
AA454375	ESTs	1.1	1.1	1.0	2.0	1.1	-1.0953+	-1.1044+	1.4	1.3	1.3	1.2	1.3
AA645046	interleukin-13	1.2	1.4	-1.2	2.0	1.5	-1.02124+	1.3	1.4	1.3	1.2	1.4	1.2

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AA030278 ESTs	1.5	1.4	-1.1	2.0	1.2	-1.22451+-	1.0	1.5	1.9	1.2	1.8	1.5
AA421164 RIKEN cDNA 489511405_gene	-1.1	1.0	-1.2	2.0	1.2	1.1	1.3	1.1	1.4	1.2	1.1	1.1
AA39091 RIKEN cDNA 281042N06_gene	1.5	1.7	1.2	2.0	1.2	-1.40231+-	1.0197+	1.3	1.9	1.2	1.7	1.5
AA574419 RIKEN cDNA 1150004M21_gene	1.1	1.4	-1.2	2.0	1.4	1.0784+-	1.3	1.4	1.3	1.3	1.4	1.3
AA027071 RIKEN cDNA 231006BA11_gene	1.5	1.4	-1.3	2.0	1.4	-1.21372+-	-1.1	1.5	1.2	1.3	1.5	1.4
AA097331 gap junction membrane channel protein beta_2	1.2	1.4	-1.1	2.0	1.2	1.17500+-	1.3	1.3	1.5	-1.2	1.1	1.0
AA4591707 DNA polymerase epsilon, subunit 2	-1.1	-1.1	1.05228+-	2.0	1.4	1.9	-1.6	1.1	1.1	-1.1	1.1	1.1
AA473552 ESTs, Moderately similar to atax DLOC1 [H.sapiens]	1.3	1.5	1.2	2.0	1.6	-1.3091+-	1.6924+	1.6	1.4	2.0	2.1181+	
AA4230774 ESTs	1.2	1.8	-1.0	2.0	1.3	-1.05003+-	-1.0	1.5	1.3	1.3	1.5	1.5
AA117905 RIKEN cDNA 853040M24_gene	-1.6	-1.1	1.6	2.0	1.4	2.3517+-	-1.3	-1.51809+-	1.3	-1.0	-1.5	-1.3
AA359824 ESTs	1.3	1.4	-1.1	2.0	1.3	-1.07451+-	1.3	1.6	1.5	1.3	1.6	1.3
AA059181 defensin related, cytidin_8	-1.8	-1.7	-1.5	2.0	1.5	2.3	-1.4	-1.2	1.1	-1.2	1.4	1.3
AA004192 RIKEN cDNA 433243K11_gene	1.2	1.4	-1.1	2.0	1.2	1.15764+-	1.2	1.2	1.2	1.1	1.4	1.8
AA050690 ESTs	1.2	1.2	-1.2	2.0	1.2	-1.18773+-	-1.2	1.6	1.4	1.3	1.5	1.3
AA473490 ESTs	1.2	1.5	-1.2	2.0	1.7	1.10148+-	1.0	1.5	1.4	1.3	1.6	1.8
AA591510 homeo box B1	-1.1	1.6	-1.4	2.0	1.7	1.80738+-	1.2	-1.0	1.2	1.1	1.1	1.3
AA073241 sulfate carrier family 22 (organic cation transporter), member 2	1.4	1.1	-1.3	1.9	1.5	-1.05070+-	1.1	1.3	1.4	1.2	1.4	1.8
AA033220 ESTs	1.2	1.8	-1.0	1.3	1.5	1.16813+-	-1.3242+-	-1.1	2.1465+-	2.0	1.6	2.57145+-
AA033220 ESTs	1.2	1.3	1.1	1.9	1.2	-1.2	-1.3	-1.0	1.4	1.3	1.1	1.3
AA007284 Kinectin 1	-1.1	-1.0	-1.3	1.8	1.7	1.50138+-	-1.6	1.1	1.3	1.0	-1.1	1.2
AA209331 ESTs	1.1	1.578+-	1.2	-1.1	1.3	1.00375+-	1.1	1.4	1.2	1.0	1.3	1.3
AA059256 chromodomain helicase DNA binding protein 1	1.4	-1.07408+-	1.0	1.3	1.1	1.34584+-	-1.85983+-	1.0	1.2	1.3	1.0	1.3
AA059256 chromodomain helicase DNA binding protein 1	1.1	-1.1	-1.0	1.3	1.3	1.1	-1.0	1.5	1.3	1.1	1.2	1.4
AA059181 JH-salivary	1.4	1.8	-1.1	1.8	1.2	-1.2	-1.2	1.4	1.4	1.3	1.6	1.55783+
AA459356 ESTs	1.1	1.1	-1.2	1.9	1.1	2.19284+-	-1.39428+-	1.1	1.4	1.1	1.4	1.2
AA028913 flyin, containing nucleoside diphosphate kinase 5	1.2	1.2	-1.13647+-	1.9	1.2	1.16925+-	1.2	1.29569+-	1.3	1.2	1.2	1.3
AA0517242 undifferentiated embryonic cell transcription factor 1	-1.5	1.5	1.6	1.9	1.4	2.17+-	1.09749+-	-1.90264+-	-1.5	-1.1	-1.8	-1.2
AA080731 nuclear factor, interleukin 3, regulated	1.4	1.2	-1.1	1.9	1.3	1.16127+-	-1.0	1.4	1.5	1.3	1.3	1.2
AA095550 leukemia/lymphoma related factor	1.2	1.4	-1.2	1.9	1.5	-1.05304+-	1.4	1.5	1.5	1.2	1.4	1.4
AA042797 hemopoietic cell signal transducer	-1.0	1.1	-1.2	1.9	1.3	1.76540+-	1.2	1.2	1.1	1.1	1.2	1.2
AA0517189 unc119 homolog (C. elegans)	1.0	1.3	1.2	1.9	1.5	-1.01509+-	1.0	-1.0	1.1	1.0	-1.1	1.1
AA097155 RIKEN cDNA 111009B06_gene	1.2	1.3	1.15501+-	1.9	1.3	-1.28546+-	1.3	1.3	1.1	1.0	1.2	1.2
AA4739464 killer cell lectin-like receptor subfamily A, member 9	1.4	1.2	-1.1	2.0	1.4	1.0592+-	1.1	1.5	1.5	1.3	1.3	1.3
AA411929 Public domain EST	-1.0	1.1	-1.4	1.9	1.3	1.33426+-	-1.1	1.4	1.5	1.2	1.3	1.4

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AA510658 ESTs	1.3	1.3	1.0	1.2	1.5	1.5	1.4	1.3	1.4	1.3
AA785388 ESTs	-1.1	1.2	-1.1	1.2	-1.0504+-	-1.0504+-	1.1	1.7	1.3	1.1
AA-58040 Public domain EST	-1.1	1.1	-1.1	1.5	1.3843+-	1.3843+-	1.1	1.2	1.3	1.1
AA477160 ESTs	1.2	1.2	-1.1	1.2	1.3189+-	1.3189+-	1.4	1.3	1.1	1.5
AA14675 ESTs	1.2	1.2	-1.1	1.4	1.2	1.2	1.2	1.2	1.1	1.0
AA50468 ESTs	1.3	1.4	-1.1	1.5	1.2	1.1	1.8	1.1	1.2	1.5
AA51472 ESTs	-1.6	1.0224+-	-1.0	1.3	1.1	1.47107+-	1.6824+-1.6	-1.2	-1.1	-1.6
AA614725 Mus musculus, clone IMAGE5404411, mRNA, perit. cells	1.1	1.2	-1.3	1.5	1.1	1.16389+-	1.1	1.1	1.2	1.3
AA60009 ESTs	1.3	1.1661+-	-1.0	1.2	1.5	1.0658+-	1.5	1.7	1.3	1.4
AA277159 RIKEN cDNA 2100075418, gene	1.0	1.5	-1.5	1.3	1.5	1.0011+-	1.4	1.3	1.1	1.2
AA604684 RIKEN cDNA 4631429C13, gene	1.2	1.3	-1.1	1.3	1.5	1.17608+-	1.5	1.4	1.1	1.2
AA168480 ESTs	1.0429+-	1.0	1.2	1.5	1.5	1.21987+-	1.1	1.2	1.1	-1.0
AA270352 ESTs	1.3	1.6	-1.3	1.3	1.3	1.02784+-	1.2	1.5	1.2	1.1
AA264772 RIKEN cDNA 241005520, gene	1.1	1.3	-1.1	1.3	1.3	1.17797+-	1.2	1.2	1.1	1.0
AA433150 nuclear localization signal protein, p45rat_1, v-erbA-erbB1, patients	-1.0	1.2	1.5	1.2	1.3	1.04778+-	1.3	1.5	1.5	1.3
AA62748 ESTs	-1.2	1.5	1.2	1.3	1.2	1.00810+-	1.03830+-	1.5	1.3	1.1
AA262871 hypothetical protein, MNC4141	-1.0	-1.0	-1.2	1.3	1.2	1.09163+-	1.1	1.5	1.3	1.2
AA107159 Mus musculus, mRNA, 161.5-b-carotene-4,10-dioxygenase (beta-oxid. genes)	1.5	1.5	1.0	1.3	1.2	-1.1	1.4	1.5	1.7	1.6
AA44659 ESTs	1.0	1.2	-1.5	1.2	1.5	-1.27048+-	1.5	1.1	1.2	1.38713+-
AA65521 ESTs	1.1	1.1	-1.0	1.2	1.2	1.32121+-	-1.3	1.3	1.4	1.1
AA514567 RIKEN cDNA 1810062J10, gene	1.3	1.4	-1.2	1.3	1.5	1.2	-1.2	1.4	1.3	1.2
AA60434 RIKEN cDNA 2010305L05, gene	1.5	1.0	1.1	1.3	1.4	1.2004+-	-1.2	1.2	1.4	1.3
AA1440 ESTs, Moderately similar to xylodiffrase [H.sapiens]	-1.2	1.2	-1.2	1.4	1.4	-1.14593+-	1.3	1.2	1.2	1.2
AA44720 ESTs	1.7	1.1	-1.8	1.3	1.2	1.11235+-	1.3	1.2	1.2	2.2
AA14454 reduced in osteosarcoma transporter	1.21144	1.1	-1.2	1.4	1.2	-1.1004+-	-1.1526+-	1.6	1.1	1.3
AA185638 ESTs	1.4	1.5	-1.2	1.3	1.1	1.3	1.4	1.3	1.1	1.4
AA60434 RIKEN cDNA 2010305L05, gene	-1.0909+-	1.10002+-	-1.07077+-	1.3	1.49564+-	1.51513+-	1.10118+-	1.1776+-	1.0384+-	1.0
AA615106 ESTs	-1.3	-1.1	1.3	1.5	1.38798+-	2.2641+-	-1.3	-1.3	-1.0	-1.4
AA628260 ESTs, Weakly similar to type III collagen [M.musculus]	1.1	1.1	-1.2	1.4	1.5	-1.26765+-	1.3	1.4	1.2	1.1
AA108049 ESTs	1.1	1.5	-1.3	1.5	1.3	1.3	1.3	1.5	1.6	1.4
AA104557 c-fos, inducible growth factor	-1.6	1.3	-1.1	1.3	1.5	-1.00294+-	1.5	1.3	1.2	1.3
AA326308 cathepsin-like protein	1.1	1.5	-1.4	1.4	1.4	-1.01691+-	1.4	1.0	1.2	1.1
AA451164 RIKEN cDNA 261001N06, gene	1.1	-1.6	1.4	1.4	1.4	1.14348+-	1.3	-1.2	1.5	1.1
AA326575 glucose-6-phosphatase, catalytic	1.3	-1.6	1.4	1.4	1.4	1.14384+-	1.4	1.5	1.2	1.1
AA59504 ESTs	1.2	1.2	-1.2	1.5	1.5	-1.14384+-	1.4	1.5	1.2	1.1

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AA38868 ESTs	1.5	1.2	1.1	1.0	1.4	-1.2144+	1.3	1.0357+	1.8	1.6132+	1.7
AA517175 Mus musculus prion, intracran. PrnT <sup>Sc</sup> , mRNA, partial cds	1.3	1.5	-1.1	-1.5	1.4	-1.3	2.0	1.6753+	1.4	1.3	1.5
AA622911 RIKEN cDNA 061009P07 gene	1.2	1.7	-1.1	1.3	1.2	-1.03749+	-1.2	1.3	1.5	1.4	1.5
AA430413 RIKEN cDNA 1700026E22 gene	1.2	-1.4	-1.2	1.5	1.3	1.3	-1.1	-1.0	1.3	-1.2	1.1
AA154791 calcitonin receptor-like	-1.1	-1.3	-1.1	1.0	1.2	-1.17718+	-1.12138+	1.3	1.1	-1.0	1.1
AA525958 RIKEN cDNA 1110009E08 gene	1.0	1.0	-1.1	1.1	1.4	-1.0763-	1.2	1.1	1.1	1.1	1.2
AA037647 Public domain EST	1.4	1.7	-1.0	1.3	1.3	-1.1	1.1	1.7	1.5	1.4	1.4
AA166466 ESTs, Weakly, similar to, T27600, hypothalamic protein, ZK620.1, Ctenorhynchus elegans [Ctenophora]	-1.2	1.1	-1.4	1.5	1.6	1.52365+	1.3	1.2	1.3	1.0	1.3
AA709728 DNA segment, Chr 3, ERATO_Dot_320, expressed	1.3	1.4	-1.0	1.5	1.2	1.07517+	1.0	1.8	1.5	1.3	1.5
AA734934 ESTs	1.26579+	1.3	-1.6	1.3	1.2	-1.06885+	-1.1	1.5	1.4	1.1	1.3
AA517891 ESTs, Weakly, similar to, E84778, probable membrane protein, viral -, Escherichia coli [Ecoli]	1.1	1.1	-1.2	1.3	1.2	-2.00749-	1.1	1.4	1.2	1.1	1.2
AA509467 ESTs, Highly, similar to, KIA00189, protein, [H sapiens]	-1.3	-1.0	-1.1	1.0	1.2	-1.26078+	-1.1	1.3	-1.1	-1.0	-1.1
AA432813 ESTs, Moderately, similar to, 161347A, est_p21, Giffers, activating protein, [M musculus]	1.2	1.2	-1.4	1.5	1.3	1.4225+	1.2	1.3	1.3	1.1	1.2
AA424503 ESTs	-1.1	1.4	-1.2	1.3	1.4	-1.07+	1.0	1.3	1.2	1.2	1.1
AA417800 actin, member 1	1.3	1.1	1.1	1.5	1.4	-1.0690+	1.3	1.04052+	1.1	1.1	1.2
AA390053 ESTs, Moderately, similar to, CYP2C10, [Mus musculus]	1.4	-1.4	-1.2	1.0	1.2	-1.07647+	1.8	1.2	1.4	1.3	1.3
AA154770 myosin family member C2	1.4	1.1	-1.0	1.5	1.2	-1.16408+	-1.47888+	1.06802+	1.2	1.0	-1.4
AA020415 identical specific protein 1	1.2	1.06017+	-1.2	1.4	1.2	-1.3	-1.3	-1.4	-1.3	-1.3	-1.2
AA414213 upstream binding protein 1	-1.1	-1.2	-1.3	-1.9	-1.4	-1.1	1.2	-1.1	-1.2	-1.1	-1.1
AA414700 actin, member 1	1.5	1.3	1.3	1.8	1.4	1.2	-1.2	-1.2	1.0	1.2	-1.2
AA783355 small EDRK-ech factor 2	1.0	-1.1	1.6	-1.9	-1.4	1.26078+	-1.3	-1.1	-1.1	-1.1	1.2
AA413854 RIKEN cDNA 1300014E15 gene	-1.0	-1.24129+	-1.7	-1.9	-1.1	1.0357+	-1.16078+	-1.12132+	-1.1	-1.2	-1.3
AA414286 RIKEN cDNA 1700018J02 gene	1.0	1.3	1.1	-1.8	1.3	1.4	-1.0	1.7	-1.1	1.0	-1.3
AA009043 glutathione peroxidase 4	1.0	-1.1	-1.0	-1.9	1.3	1.4	1.1	1.1	1.1	1.2	-1.1
AA238171 protein phosphatase 2, [formerly 2A], regulatory, subunit A, [P85], alpha isoform	1.0	-1.1	-1.0	-1.9	1.3	1.4	1.1	1.1	1.1	1.2	-1.1
AA752870 RNA-associated invariant chain	1.0	-1.8	-1.6	-1.9	1.5	3.7	-2.8	-1.0	1.9	-1.0	-1.3
W83121 leupathin	1.2	-1.5	1.1	-1.8	-1.0	-1.7	-1.0	-1.3	-1.1	1.2	-1.3
AA94339 nuclear factor IC	1.3	-1.2	-1.2	-1.9	1.0	1.1	-1.2	-1.0	-1.3	-1.2	-1.4
AA116934 monoclonal antibody	-1.5	-1.1	-1.1	-1.9	-1.1	1.6	-1.3	-1.2	-1.3	-1.3	-1.2
AA671029 PKC06 binding protein 4, [99 kDa]	-1.1	1.2	1.0	-1.8	-1.4	-1.4	-1.7	-1.0	-1.1	-1.1	-1.2
AA414514 microtubule-associated protein, RPEB family, member 1	1.0	-1.3	-1.1	-1.9	-1.2	1.4	1.3	1.0	1.1	-1.1	-1.0
AA08465 cdc42, G	-1.2	1.0	1.3	-1.9	-1.8	2.28073+	1.2	-1.4	-1.4	-2.0	-1.0
AA045400 claudin 4	-1.6	1.5	-2.1	-1.9	1.8	2.7	1.5	-1.1	-1.2	-1.3	-1.2



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AA781818 aminexin A5	1.3	-1.4	1.1	-1.9	-1.0	-1.0	1.2	1.1	-1.1	1.0	-1.1
AA465997 RIKEN cDNA 2010103A03 gene	1.2	1.2	1.1	-1.9	-1.2	-1.5	1.1	1.2	1.0	-1.2	1.0
AA363340 glutathione peroxidase 2, pseudogene 1	-1.3	-1.0	1.2	-1.9	1.1	-2.4	-2.5	-1.5	1.1	-1.1	-1.5
AA415520 RIKEN cDNA 311003B024 gene	1.2	1.2	-1.1	-1.9	-1.1	-1.422274	1.1	1.3	1.2	1.0	-1.0
AA120679 RIKEN cDNA 311009E09 gene	1.2	1.3	1.1	-1.9	-1.6	-1.3	1.0	1.8	-1.1	-1.2	-1.5
AA106736 cytochrome c oxidase, subunit VIIa 3	1.1	-1.0	1.6	-1.9	-1.2	-1.1	1.0	1.3	1.0	-1.2	-1.1
AA414844 emerin	1.3	1.4	-1.0	-1.9	1.1	-1.0	-1.1	1.1	-1.0	1.1	-1.1
AA176807 syntaxin6/8/9	-1.6	-1.3	-1.5	-1.9	-1.3	-1.3	1.4	-1.7	-1.5	-1.3	-1.2
AA154947 ESTs	-1.3	-1.5	-1.1	-1.6	-1.1	-1.0	-1.1	-1.1	-1.2	-1.1	-1.2
W15971, FK506 binding protein 2 (13 kDa)	-1.0	-1.0	-1.1	-1.9	-1.2	-1.4	-1.2	-1.4	-1.3	-1.0	-1.1
AA051479 Public domain EST	-1.2	-1.6	-1.1	-1.9	-1.6	-1.1	-1.1	-1.3	-1.2	-1.3	-1.2
AA009409 histone-related protein complex AP-3, sigma 2 subunit	-1.5	-1.3	-1.3	-1.9	-1.1	-1.2	-1.0	-1.1	-1.2	-1.1	-1.2
W54952, glutathione S-transferase, mu 6	1.2	1.1	1.5	-1.9	-1.3	1.2	1.2	-1.1	1.1	1.3	-1.0
AA322387 insulin-like growth factor 2	-1.2	1.6	-1.4	-1.9	-1.5	1.4	-1.5	-2.0	-1.2	-1.8	-1.2
AA727850 keratin complex 1, acidic, gene 18	1.0	1.5	-1.2	-1.9	-1.1	1.0	-1.7	-1.0	1.1	-1.2	-1.0
AA92334, ribosomal protein L5	1.3	1.4	1.1	-1.9	-1.2	1.1	1.2	1.1	1.3	-1.2	-1.1
AA329371 heat shock protein, 88 kDa 1	1.4	1.0	-1.3	-1.9	-1.9	-1.5	1.4	1.3	1.2	-1.0	-1.3
AA671749 ESTs, Weakly similar to I46759 Hrs - mouse [Mus musculus]	-1.5	-1.2	-1.4	-1.9	-1.1	-1.4	1.3	-1.4	-1.4	-1.5	-1.1
AB45415, mini chromosome maintenance deficient (S. cerevisiae)	1.1	1.6	-1.3	-1.9	-1.4	-1.2	-1.8	-1.4	-1.2	-1.2	-1.3
AA415905 nucleolar and colloid-body phosphoprotein 1	1.1	1.4	1.3	-1.9	-1.2	-1.0	-1.4	-1.0	-1.0	1.1	-1.1
AA29586 RIKEN cDNA 311009B05 gene	-1.3	-1.5	-1.2	-1.9	-1.2	1.4	1.0	-1.3	-1.4	-1.1	-1.4
AA087069 histocompatibility 2, T region locus 9	1.2	-1.2	1.8	-1.9	-1.4	-1.3	1.1	-1.1	-1.1	1.1	-1.0
AA674445 lectin, galactose binding, soluble 9	-1.4	-1.0	1.6	-1.9	-1.2	-1.7	-1.4	-1.0	1.3	-1.2	-1.0
AA003005 CD151, antigen	-1.4	-1.5	-1.3	-1.9	-1.1	-1.3	-1.2	-1.2	-1.4	-1.1	-1.2
AA181802 RIKEN cDNA 3021401A05 gene	-1.1	-1.1	1.2	-1.9	-1.6	-1.2	-1.5	1.1	-1.1	-1.2	-1.1
AA52472 RIKEN cDNA 061001C08 gene	-2.0	-2.1	-1.6	-1.9	-1.5	-1.3	-1.3	-1.9	-1.8	-1.5	-1.7
AA35457 retino binding protein 2, cellular	-1.1	-1.2	-1.3	-1.9	-1.1	-1.2	-2.240494	-1.0	1.1	-1.3	-1.1
AA049438 torin family 3, member A	-1.0	2.0	1.1	-1.9	1.1	-1.2	1.2	1.0	1.1	1.4	1.0
AA442020 Public domain EST	1.4	1.2	-1.0	-1.9	-1.3	-2.3	1.0	-1.1	1.0	-1.1	1.1
AA097896 0.6-methylguanine-DNA methyltransferase	-1.2	1.2	-1.6	-1.9	-1.3	-1.2	-1.7	-1.9	-1.1	-1.2	-1.1
AA240606 RIKEN cDNA 261020H419 gene	-1.0	-1.2	1.3	-1.9	-1.3	1.2	-1.7	-1.9	-1.1	1.0	-1.4
AA619850 cyclin 1	-1.1	-1.2	1.1	-1.9	-1.1	-1.1	1.5	-1.4	-1.3	1.1	-1.1
AA250037 proteasome (prosome, macropain) subunit, beta type 8 (large multifunctional protease 7)	1.1	1.5	1.1	-1.9	1.0	-1.2	-1.5	-1.2	1.1	1.2	-1.0

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AA030661	kinase light chain 2	-13	-14	-14	-15	-11	-14	12	-14	-14	-12	-12	-12
AA062981	botulin	-12	-11	-13	-13	13	212552	-12	13	10	11	-12	-14
W10007	mast cell protease 6	-12	-14	-13	-13	-12	-12	-14	-12	-13	-13	-14	-14
AA468867	tumor necrosis antigen gp66	-13	14	-15	-19	-20	-14	12	-11	12	-11	11	-10
AA4684310	protein tyrosine phosphatase 4s1	-12	11	12	-20	-16	-12	13	11	10	-10	11	-11
AA453118	ESTs	-18	-12	-14	-20	11	-13	-11	-13	-15	-13	-12	10
AA500739	potassium channel, subfamily K, member 2	-11	-10	11	-20	-17	-124216	-14	-10	-10	-13	-10	-12
AA460361	rhomboid protein 144	-13	14	13	-20	-17	-12	12	-14	-10	-12	-14	-10
AA684403	ESTs	-14	17	-23	-20	20	24	15	10	-13	-13	-11	-11
AA680337	inactive X specific transcripts	13	-104285	13	-20	-13	115378	-13394	-12	-15	12	-13	-12
AA261440	lymphocyte-associated peptide 1	12	10	17	-20	-14	-11	11	-16	-10	11	-10	-12
W03321	inhibitor of DNA binding 1	11	-11	11	-20	-11	27	-18	-11	-10	10	-10	12
AA116336	transducer of ErbB-2.1	-10	-12	13	-20	-19	-11	11	-12	-11	-10	-12	12
AA437763	glycyl ras-related homodimer B (RasB)	-12	-16	-12	-20	-10	15	10	-12	-11	-14	-13	-12
AA037003	guanine S-transferase, mu 1	11	12	10	-20	15	19	14	10	12	14	-13	-12
AA068583	bradykinin dehydrogenase 2, B chain	12	12	133999	-20	-13	14	13	10	13	16	12	-11
AA060959	actin, gamma, cytoplasmic	11	-12	-11	-20	-10	-14	14	11	11	12	10	-10
AI121405	H2O-like homodimer box gene	-17	-16	-12	-20	-11	16	-12	-12	-15	-13	-13	-13
AA437457	methionine aminopeptidase	13	-10	12	-20	-11	-11	-14	-10	10	-10	-10	-11
W17786	serine protease, class 10, homolog (human)	10	-11	-11	-20	-10	-11	12	-17	-10	-11	-12	-10
AA118994	diacylglycerol binding inhibitor	-12	13	-11	-20	-11	-13	-12	-12	-12	11	-12	-13
AI184712	ESTs	12	12	14	-20	-10	13	14	-13	-10	-11	-12	-11
AI893237	RKEN cDNA 081008D10, gene	-17	-13	-14	-20	-11	-13128	-12	-14	-14	-12	-12	-12
AA874602	ESTs	-16	-17	-14	-20	-14	-14	-12	-14	-14	-14	-12	-12
AA620001	ESTs	-14	14	-15	-20	-11	-13	11	-13	-15	-13	-11	-12
AA874467	RKEN cDNA 1100356307, gene	23	15	-13	-20	-15	-13	16	-15	-20	-14	-11	-11
AA982254	RKEN cDNA 221010004, gene	11	11	11	-20	-20	11	-12	-15	-12	-14	-13	-11
AI527415	Mus musculus, clone MSC6848, mRNA, complete cds	-16	-16	-11	-20	-11	-11	-12	-15	-14	-13	-11	-11
AA734030	oidid receptor, sigma 1	-18	-12	106597	-20	-12	13	-11	-11	-11	-11	-11	10
AA926103	max binding protein	-18	-15	-14	-20	-13	-12	-11	-13	-18	-15	-15	-16
AA174675	ESTs	-18	-14	-12	-20	-11	-13	-13	-14	-14	-13	-13	11
AA586002	ESTs	-18	-16	-16	-20	-12	-14	-11	-11	-15	-13	-12	-13
W13008	antihistaminic peptide receptor 1	-18	-16	-16	-20	-12	-14	-11	-11	-15	-13	-12	-13
AA210481	classen	11	30	12	-20	-16	-14	13	-11	11	14	-12	12

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AA082482 ESTs. Moderately similar to C2H1 human putative SURF	1.1	1.1	1.3	-2.0	-1.1	1.1	1.3	-1.2	-1.2	1.4	-1.1	1.1
ACE_GLYCOPOLIN_C2H1P1_PRCURSOR_Hs[aligns]												
AA390138 RIKEN cDNA 353404B19. gene	-1.4	-0.7	-1.1	-2.0	-1.2	-2.1	-1.3	-1.2	1.5	-1.9	-1.3	-1.1
AA347494 Public domain EST	1.0	1.093+	1.4	-2.0	-1.2	-1.6479+	1.31017+	-1.3034+	1.1	-1.3	-1.0	1.2
W33489. aminoacidin	1.2	1.2	1.1	-2.0	1.1	-1.3	1.1	-1.1	1.0	1.1	-1.2	-1.0
AA330970 RIKEN cDNA 231020P24. gene	-1.6	-1.5	-4.5	-2.0	-1.1	-1.36736+	-1.0	-1.3	-1.3	-1.5	-1.3	-1.4
AA57633 RIKEN cDNA 2710401F7. gene	-1.2	-1.2	1.4	-2.8	-1.1	1.0	-1.3	-1.7	-1.1	1.1	-1.2	-1.2
AA711419 POU domain, class 2, transcription factor 1	1.3	1.4	1.1	-2.0	1.1	-1.0813+	-1.4	1.0	-1.2	-1.2	-1.1	-1.1
AA119836 myxovirus (influenza virus) resistance 1	1.0334+	-1.6994+	-1.39873+	-2.0	-1.10242+	1.10979+	-1.00713+	1.1	-1.1	-1.1	1.1	-1.8
AA42782 ESTs	-1.4	-1.3	-1.2	-2.0	-1.3	-1.2	-1.0	-1.1	-1.3	-1.2	-1.2	-1.2
AA329209 ribosomal protein L27a	1.5	1.1	1.3	-2.0	-1.5	1.0	1.2	-1.1	1.1	1.0	-1.2	-1.0
AA556665 Fibroblast growth factor 10, murine sarcoma virus (FBR)	1.2	1.4	1.1	-2.0	1.1	-	-1.1	-1.2	-1.1	1.0	-1.3	-1.0
MA5V1. chikungunya virus, expressed (for Jiv'nes)	-1.6	-1.6	-1.2	-2.0	-1.2	-1.0	-1.1	-1.1	-1.4	-1.3	-1.3	-1.2
AA466951 RIKEN cDNA 913012E05. gene	1.3	1.0	1.2	-2.0	-1.8	-1.2	-1.1	-1.2	-1.2	-1.1	-1.1	-1.1
AA241408 polyomavirus alpha	-1.4	-1.4	-1.2	-2.0	-1.4	-1.3	-1.1	-1.2	-1.4	-1.6	-1.1	-1.1
AA711675 unt. related transcription factor 2	1.2	1.3	1.0	-2.0	1.2	-1.1	-3.5	-1.5	1.1	-1.1	-1.3	-1.4
W18330. topomycin 2, beta	1.1	1.4	-1.1	-2.0	1.5	-1.1	1.3	1.2	1.1	-1.0	-1.0	-1.2
AA004650 calmodulin	-1.1	1.8	-1.2	-2.0	-5.21	-1.8977+	-1.4	1.0	-1.4	-1.9	-1.0	1.4
AA94032. insulin factor 2 (insulinolytic protein 1)	1.1	1.1	1.7	-2.0	1.3	-1.1	1.2	-1.1	1.2	1.2	-1.1	-1.0
AA106338 Public domain EST	-1.4	1.0	-1.2	-2.0	1.0	-1.28739+	-1.0	-1.3	-1.3	-1.2	-1.3	1.0
AA414427 RIKEN cDNA 943015P0. gene	1.3	1.2	1.4	-2.0	-1.8	-1.2	1.1	-1.0	1.1	-1.1	1.0	-1.0
AA176784 ESTs	-1.3	1.02041+	-1.1	-2.0	-1.1	-1.20277+	-1.05224+	1.08168+	-1.0	1.0	1.2	1.4
AA026283 peptidase (amylase) protein	-1.2	1.4	1.1	-2.0	-1.3	-1.4	-1.3	-1.4	1.0	-1.1	-1.2	1.0
AA414118 signal recognition particle 9.1Da	-1.4	-1.9	-1.3	-2.1	1.0	-1.1	-1.2	-1.2	-1.4	-1.0	-1.1	-1.2
AA026283 peptidase (amylase) protein	1.3	1.7	1.2	-2.1	1.1	-1.3	1.8	-1.1	1.2	1.3	-1.0	-1.0
AA444231 ribosomal protein S5	-1.7	-1.6	-1.3	-2.1	-1.1	-1.1	-1.1	-1.4	-1.2	-1.1	-1.3	-1.2
AA119056 Public domain EST	1.2	-1.2	1.1	-2.1	1.1	-1.6	-1.0	1.1	1.0	-1.0	-1.0	-1.0
AA419820 EST AA598854	1.2	-1.2	1.1	-2.1	1.1	-1.6	-1.0	1.1	1.0	1.1	-1.0	1.1
AA711682 insulin VI	1.1	-1.2	-1.0	-2.1	-1.2	1.1	1.1	1.0	1.1	1.1	-1.0	1.1
AA583832 G. protein-coupled receptor, family C, group 5, member B	-1.3	-1.7	-1.4	-2.1	-2.9	-1.3	-1.6	-1.1	-1.3	-1.1	-1.1	-1.0
AB048485 (inquin-like) (antimicrobial) activating enzyme E1A	-1.4	-1.5	-2.1	-1.2	1.20761+	-1.4	1.0	-1.5	-1.4	-1.4	-1.3	-1.2
W14844. Public domain EST	-1.2	-1.3	-1.2	-2.1	1.0	1.2	-1.0	-1.0	-1.1	1.1	-1.2	-1.3
AA019602 ribosomal protein L3	1.0	1.4	1.3	-2.1	-1.1	-1.0	1.1	-1.3	1.0	1.1	-1.4	-1.0
AA545514 interferon gamma induced GTPase	1.2	-1.1	1.5	-2.1	-1.2	-1.39378+	-1.6	-1.6	1.0	1.2	-1.2	1.1
AB501147 beta-2 microglobulin	1.8	1.1	1.2	-2.1	2.0	-1.6	-1.0	-1.1	-1.0	1.3	-1.1	-1.2
AA326556 FMS-like tyrosine kinase 1	1.1	-1.3	1.5	-2.1	-1.1	1.0	1.1	-1.0	-1.3	1.2	-1.6	-1.5

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AA38309	RKEN cDNA 22104101.06 gene	-1.8	-1.8	-1.4	-2.1	-1.9	1.1	-1.5	-2.0	-1.6	-2.1	-1.5	-2.1
AA06787	nest shock protein coplate 70	-1.0	-1.1	-1.0	-2.1	-2.1	-1.5	-1.1	1.3	1.5	1.3	1.0	1.2
AA27281	protein kinase C and casein kinase substrate in neurons 2	-1.4	-1.2	-1.3	-2.1	-1.2	-1.4	-1.6	-1.1	-1.3	-1.2	-1.3	-1.2
AA82534	ribosomal protein S21	1.3	1.1	1.3	-2.1	-2.0	-1.1	1.3	-1.2	1.2	-1.4	-1.1	-1.2
AA79876	specin, lymphocyte	-1.7	-1.5	-1.2	-2.1	-1.0	-1.2	1.0	-1.5	-1.6	-1.5	-1.5	-1.4
AA182180	thres prime, repair exonuclease 1	-1.4	-1.1	-1.1	-2.1	1.0	-1.26936	-1.4	1.2	-1.0	1.0	-1.0	-1.1
AA107102	proble stem cell antigen	-1.1	-1.4	-1.3	-2.1	-6.1	1.51614	-1.8	-2.1	-1.0	-1.1	-1.4	-1.4
AA43784	glutathione S-transferase p1.2	1.1	1.5	1.2	-2.1	1.5	1.4	1.1	-1.6	1.1	1.1	-1.5	-1.2
AA27409	microsomal triglyceride transfer protein	-1.7	-1.4	-1.4	-2.1	1.0	1.2	1.0	-1.6	-1.3	-1.3	-1.4	-1.3
AA46728	RKEN cDNA 1700080222 gene	-1.4	-1.6	-1.5	-2.1	-1.2	-1.2	1.0	-1.5	-1.4	-1.1	-1.4	-1.3
AA71285	protease (prosome, macrogulin) 28 subunit 3	-1.2	-1.0	1.4	-2.1	-1.2	-1.5	-1.3	-1.4	-1.0	1.1	-1.2	-1.1
AA312150	ectodermal transcription factor 1 alpha 1	1.1	-1.3	-1.3	-2.1	1.1	-1.1	-1.0	-1.1	-1.1	1.0	-1.1	-1.3
AA62247	glutathione S-transferase, alpha 1 (N)	-1.1	-1.3	-1.7	-2.1	-1.7	-2.0	-1.2	-1.1	1.4	1.8	-1.1	1.1
AA66790	topogin 1, cardiac	1.4	-1.6	-1.1	-2.1	1.3	1.41207	-2.0	-2.0	-2.2	3.55728	-1.0	1.3
AA072854	RKEN cDNA 9035418005 gene	1.1	1.2	-1.1	-2.1	1.33144	-3.3	-1.1	1.1	-1.1	1.1	1.1	1.3
AA42838	ESTs	-1.6	-1.7	-1.4	-2.1	-1.3	-1.3	-1.2	-1.2	-1.5	-1.2	-1.3	-1.2
AA49839	RKEN cDNA 251031025 gene	-1.1	1.6	-1.2	-2.1	-1.1	-1.1	1.3	-1.1	1.0	1.1	-1.2	1.1
AA075114	RKEN cDNA 1810070424 gene	1.4	1.3	-1.0	-2.1	-1.0	-1.5	1.0	-1.4	-2.2	-1.2	-1.2	-2.0
AA23198	lunar necrosis factor receptor superfamily, member 4	-1.3	1.2	1.1	-2.1	-1.2	-1.46523	1.1	-1.1	-1.2	-1.1	-1.3	-1.3
AA17056	ESTs	1.1	-1.2	1.2	-2.1	-2.5	1.2	-1.2	-1.6	-1.2	-1.4	-1.4	-1.3
AA13842	Public domain EST	-1.1	-1.1	-1.0	-2.1	1.2	1.0	1.6	1.4	1.1	1.1	1.7	1.4
AA66534	salivary 10	1.1	1.0	1.2	-2.1	1.2	1.1	1.1	-1.1	1.4	-1.2	-1.0	-1.2
AA47487	RKEN cDNA 1110038014 gene	-1.1	1.3	-1.1	-2.1	1.2	1.5	-1.3	-2.1	-1.4	-1.4	-1.8	-1.2
AA21056	Public domain EST	1.4	-1.5	1.2	-2.1	-2.7	-1.7	-1.1	1.1	1.3	1.1	1.1	1.2
AA12007	2.5' oligodeoxynucleotide synthetase-like	1.1	-1.4	-1.3	-2.1	-1.1	-2.2	-1.1	1.3	-1.1	-1.1	-1.1	-1.1
AA007044	RKEN cDNA 270008919 gene	-1.4	-1.3	-1.5	-2.1	-1.0	-1.4	-1.1	-1.4	-1.3	-1.3	-1.3	-1.9
AA047891	RKEN cDNA 2700041622 gene	-1.1	1.3	-1.1	-2.1	-1.0	-1.0	-1.3	-1.4	-1.4	-1.3	-1.4	-1.2
AA11185	fibronectin protein S15	-1.1	1.1	-1.2	-2.1	-1.0	-1.2	1.2	-1.3	-1.3	-1.1	-1.2	-1.2
AA76566	potassium voltage-gated channel, subfamily O, member 1	1.2	1.6394	1.3	-1.42723	2.2	1.0	1.08561	-1.33259	1.314339	1.05921	1.1	-1.01648
AA37894	beta2-microglobulin (AP) repeat-containing 4	-1.6	-1.5	-1.5	-2.1	-1.2	-1.2	-1.2	-1.2	-1.2	-1.2	-1.2	-1.2
AA616180	RKEN cDNA 2010004812 gene	-1.2	1.2	1.2	-2.1	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4	-1.4
AA18359	multi-1, transmembrane	1.5	1.4	-1.2	-2.1	-1.3	-1.1	-2.0	1.0	1.1	1.1	-1.2	1.0
AA546025	ESTs, Weakly similar to SPB2_MOUSE SPULCOSOME_ASSOCIATED PROTEIN (B2.Musculi)	-1.9	-1.6	-1.4	-2.1	-1.2	-1.4	1.2	-1.2	-1.7	-1.7	-1.4	-1.6

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AA068845	vitin 2	-10	-13	13	22	13	12	-12	4.1	-1.2	1.1	-1.1	-1.0
AA047184	Mus myosin, myos protein, (b2sp), genes, complete cds	-18	-19	-22	-22	-10	-11	-12	4.4	-1.8	-1.8	-1.8	-1.6
AA045002	atf-70D protein 5 (glucose-regulated protein, 78kD)	1	16	24	22	24	-1.6	10	4.3	1.2	-1.1	-1.1	-1.2
AA060105	trifol f1c1	-15	-14	13	22	-43.1148*	-1.00853*	10	4.2	-1.6	1.0	-1.0	-1.5
U939311	epoxyacyl isomerase, C-associated protein	11	-10	14	-22	-12	11	11	4.0	1.3	1.1	-1.1	-1.1
		-11	-12	11	22	11	1.1	-12	4.5	-1.1	1.4	-1.2	-1.2
		-11	-12	12	22	22	10	-12	4.6	-1.2	-1.5	-1.3	-1.2
AA068404	topoisomerase (CNA) II beta	-18	-18	-13	-22	-12	1.3	13	3.6	-1.5	-1.2	-1.3	-1.3
AA067948	RKEN, CDNA, 1110015B/005 genes	-18	-19	-13	22	-12	-10	-13	4.4	-1.5	-1.2	-1.4	-1.5
AA087765	potassium voltage-gated channel, Isk-related subfamily, member 1	-19	-18	-15	22	-12	-1.47043*	-1.53147*	4.5	-1.6	-1.5	-1.4	-1.5
	AA43757 ESTs												
AA028066	ATP synthase, H <sup>+</sup> transporting, mitochondrial F0 complex, subunit g	11	-10	16	22	-14	-12	-12	4.7	-1.1	-1.3	-1.2	-1.3
	built g												
AA181582	foslike antigen 2	-21	-20	-14	-22	-12	-11	-13	4.4	-1.4	-1.4	-1.4	-1.5
AA069202	small inducible cytokine subfamily B (Cys-X-Cys), member 14	-15	-17	-14	-23	-11	-10	-11	-1.4	-1.4	-1.5	-1.3	-1.2
	small inducible cytokine subfamily B (Cys-X-Cys), member 14												
AA242902	ESTs	-19	-13	-14	-23	10	-14	-11	-1.3	-1.6	-1.5	-1.4	-1.4
		-10	11	14	-23	-13	1.21428*	-12	-1.1	1.2	1.1	-1.1	-1.0
AA108615	RKEN, CDNA, 09100770/0 genes	-15	-15	-19	-23	13	-10	14	-20	-1.5	-1.4	-1.3	-1.5
U92207	neurot specific gene family member 2	10	-12	-23	12	-10	-13	-10	1.1	-1.0	1.3	1.6	1.6
AA020170	serum, hemoglobin, immunoglobulin domain, (Ig), transmembrane, do main (TM) and short cytoplasmic domain, (transmembrane) 4D	-14	-15	-16	-23	-11	-12	-12	-1.5	-1.5	-1.1	-1.2	-1.0
AA477003	peisigargin receptor isoform 1	-19	-21	-16	-23	-11	-12	-10	-1.5	-1.6	-1.5	-1.6	-1.8
		11	10	13	-23	-12	-10	-12	-1.1	1.1	1.0	-1.1	-1.0
AA052203	cytochrome c oxidase, subunit Va	-14	-13	-13	-23	-14	-14	-12	-1.1	-1.3	-1.5	-1.1	-1.1
U98524	schlafen 2	-12	-13	-23	-13	12	11	14	-1.1	-1.4	-1.1	-1.1	-1.1
AA010514	RKEN, CDNA, 13000032/09 genes	-12	-12	-15	-23	-11	-15	-11	1.1	-1.4	-1.4	-1.2	-1.2
AA090037	Kuppelless, factor 2 (lup)	-13	-14	-14	-23	-11	-15	-11	1.1	-1.4	-1.4	-1.2	-1.2
AA048653	RAD51, line 3 (S. cerevisiae)	-17	-15	-15	-23	-11	-15	-13	-1.3	-1.5	-1.2	-1.3	-1.3
AA017049	methionine sulfoxide reductase, with teratopogadile repeats 1	-11	-12	-11	23	-16	-1.20628*	-14	10	-1.1	-1.2	1.1	-1.1
U92495	anxinin A10	15	-17	-11	23	-8.5	-1.85667*	-14	1.1	-1.0	1.0	-1.0	-1.9
AA113501	ATP synthase, H <sup>+</sup> transporting, mitochondrial F1F0 complex, subunit e	14	11	15	23	-14	-10	1.0	-1.7	-1.1	1.1	-1.2	-1.4
	subunit e												
AA014006	gene rich cluster, C9 gene	-17	-14	-15	-23	-11	-13	11	-1.5	-1.5	-1.2	-1.4	-1.3
AA176997	carboxyl ester lipase	15	18	-14	-23	-8.9	-1.4	-1.1	1.1	-1.4	-1.1	1.1	2.0
AA444672	RKEN, CDNA, 2510001A/17 genes	-11	-10	11	23	-20	-1.1	1.3	-1.1	1.2	-1.4	1.0	-1.2
AA040003	heterogeneous non-abundant protein D	-10	-8	-16	-23	-11	-12	-12	-1.3	-1.3	-1.2	-1.3	-1.5
A125332	polyubiquitinase 3, E polypeptide	-20	-20	-14	-23	-12	-12	-12	-1.2	-1.2	-1.7	-1.4	-1.5
	crossed subunit, S. cerevisiae, alpha 4	11	10	18	24	-30	1.3	12	10	1.3	1.3	-1.1	-1.2

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AA822038, andropodrin A-1	-1.9	-1.5	1.1	-2.4	2.1	2.4	-1.9	-4.0	-1.2	-2.1	-2.5	-1.6
AA616848, RIKEN cDNA 443042C14, gene	1.5	-1.3	-1.1	-2.4	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1	-1.1
AA561014, EST	-1.6	-1.6	-1.4	-2.4	-1.2	-1.5	-1.3	-1.4	-1.5	-1.4	-1.5	-1.3
AB583751, EST, Highly similar to AF091157_1 zinc finger protein_RIN_Z (R. IR ungrouped)	1.5	-1.2	-1.0	-2.4	-1.0	-1.0	-1.1	-1.1	-1.0	-1.1	-1.0	-1.1
AA719478, RIKEN cDNA 081025G13, gene	1.2	1.6	1.3	-2.5	1.1	-1.1	-1.1	-1.4	-1.0	1.2	-1.3	1.2
AA470709, aldehyde dehydrogenase family 3, subfamily A1	-1.1	1.1	-1.2	-2.6	1.3	-1.6108-	1.5	-4.0	-1.0	1.1	1.4	1.3
AA437826, RIKEN cDNA 181005E05, gene	-1.4	-1.6	-1.4	-2.6	-1.2	-1.0	-1.1	-1.3	-1.5	-1.3	-1.3	-1.2
AA727827, arylamidase 1, arylamidase	-1.6	-2.1	-1.6	-2.5	-1.3	-1.2	-1.4	-1.4	-1.6	-1.6	-1.4	-1.7
AA516482, RIKEN cDNA 091000A18, gene	1.8	1.3	-1.1	-2.5	-1.67	-2.6	1.2	-1.3	-2.4	-1.3	-1.1	-1.3
W15606, cytochrome, beta, heavy chain, 11	1.3	-1.3	-1.1	-2.5	-2.1	-1.8	-1.1	1.0	-1.1	-1.2	-1.2	-1.1
AA437871, eukaryotic translation initiation factor 4, gamma 2	-1.1	1.0	1.4	-2.5	-1.7	-1.0	1.2	-1.0	1.2	1.1	-1.0	1.1
AA183971, zinc finger protein, 67	-1.8	-1.8	-1.4	-2.6	-1.2	-1.2	-1.3	-1.3	-1.5	-1.5	-1.4	-1.4
AA194146, ribosomal protein S19	1.2	1.1	1.2	-2.5	-1.4	-1.0	1.1	-1.4	-1.0	-1.1	-1.3	-1.1
AA044852, soluble carrier family 4, anion exchange, member 2	-1.0	1.1	1.1	-2.5	-1.1	-1.5	-1.4	-1.0	-1.3	-1.0	-1.2	-1.0
AA444254, ornithine decarboxylase, structural	1.2	-1.0107+	-1.1	-2.5	1.3	-1.3814+	1.4	1.1	1.1	1.1	1.1	1.1
AA17532, thymidine kinase, family LPS-inducible, member	1.1	-1.3	-1.4	-2.6	-1.6	-1.2	-1.1	-1.6	-1.4	-1.1	-1.1	-1.0
AA444254, ornithine decarboxylase, structural	1.3	-1.3	-1.1	-2.6	1.1	-1.2	-1.8888-	-1.2	-1.0	-1.1	-1.1	1.0
AA172517, interferon regulatory factor 7	1.3	-1.3	-1.1	-2.6	1.1	-1.2	-1.1	-1.0	-1.2	1.1	-1.2	1.1
AA322733, 2,5-dipadenosine synthetase 1A	1.3	1.3	1.4	-2.6	-1.2	-1.2	-1.0	-1.3	1.1	-1.0	-1.1	-1.0
AA082440, coding	1.0	1.5	1.1	-2.6	1.2	-1.1	1.4	-1.1	1.2	1.2	-1.1	-1.1
AA245976, ethylphosphamide dehydrogenase	-1.1	1.0	1.2	-2.6	-1.8	1.3	-1.1	-1.0	-1.2	-1.3	-1.0	1.1
AA151676, ESTs	1.1	1.1	-1.2	-2.7	-2.5	-3.2	-2.1	-1.6	-2.9	1.2	-1.1	-1.4
AA717026, Myo, myosin, 10, 300, and myosin paracetamol cDNA, RIKEN full-length, ungrouped library, gene 101026A117, 3' UTR, direct sequence	-1.9	-1.6	-1.6	-2.7	-1.1	-1.5	-1.0	-1.6	-1.7	-1.6	-1.5	-1.6
AA494778, ESTs	-1.1	-1.1	-1.1	-2.7	-1.6	-1.6	-1.5	-1.6	-1.5	-1.6	-1.6	-1.4
AA674270, major urinary protein 1	-1.3	-1.1	-1.1	-2.7	-1.6	-1.6	-1.5	-1.6	-1.5	-1.6	-1.6	-1.4
AA175605, RIKEN cDNA 579345P16, gene	2.3	1.4	-1.2	-2.7	-2.1	-2.2	-1.7	-1.6	-1.4	-1.4	-1.2	-1.4
AA675504, classmate 2	-1.3	-1.6	-1.0793-	-2.7	1.0	1.1	1.1	-1.4	1.0	1.3	-1.3	1.0
AA555605, ribosomal protein L28	1.3	1.2	-1.6	-2.8	-1.7	-2.1	1.1	-1.2	-1.0	-1.0	-1.4	1.1
AA126876, CD24a antigen	-2.1	-2.2	-1.6	-2.8	-1.3	-1.6	-1.2	-1.7	-2.0	-1.7	-1.6	-1.8
AA414790, leukotriene A4 hydrolase	8.1	1.1	-1.2	-2.8	-32.0	-4.0	2.8	-1.2	-4.4	-1.1	-1.1	-1.2
AA421894, myosin 2, pancreatic	1.0	1.0	-1.1	-2.8	-1.0	-1.8914-	1.0733+	1.2	1.1	1.1	1.1	1.1
AA185652, RIKEN cDNA 261000A-01, gene	2.0	2.2	-1.6	-2.9	-1.3	-1.3	-1.2	-1.6	-1.7	-1.8	-1.7	-1.8
AA73740, ESTs	1.5	-1.2	1.2	-2.9	1.3	3.7	2.1	-1.2	-1.0	-1.0	-1.7	-1.8
W15609, hemoglobin, beta adult, major chain	1.3	-1.4	1.3	-3.0	-1.5	-1.2	-2.8	-1.2	-1.3	-1.0	-1.3	-1.2
AA122791, Nalcompatibility 2_Q region, locus 7	1.3	-1.4	1.3	-3.0	-1.5	-1.2	-2.8	-1.2	-1.3	-1.0	-1.3	-1.2

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AA119071	hemoglobin, beta adult major chain	1.3	-1.4	1.2	-3.0	-1.1	4.3	2.7	1.1	-1.3	1.8	-1.7	-2.0
W14853	kinin-associated protein, 3	-1.0	-1.0	1.4	-3.2	-1.2	-3.5332~	3.3	-1.2	-1.2	1.3	-1.5	-1.5
AA272519	interferon-induced protein with leucine-rich repeats 3	1.3	-1.1	1.1	-3.3	1.2	1.53884~	-1.2	1.2	-1.0	-1.3	-1.1	-1.2
A102498	glycosylphosphatidylinositol-specific phospholipase D1	1.1	-1.3	1.2	-3.4	2.3	-1.5	2.3	1.2	-1.3	1.2	-1.6	-1.6
A1324722	lymphocyte antigen 6 complex, locus E	-1.1	-1.2	-1.2	-3.5	-1.1	-2.0	1.1	-1.1	-1.1	-1.4	1.1	-1.2
AA390958	ubiquitin-specific protease 18	1.1	1.0	1.2	-3.8	1.1	-2.26833~	1.2	1.1	1.1	1.0	-1.1	-1.2
AA327769	cf. regenerating liver-derived mouse homolog 1	2.4	1.4	-1.3	-3.9	-11.8	-2.2	1.0	-1.4	-2.7	-1.2	-1.2	-1.2
AA095763	hemoglobin, beta adult major chain	1.3	-1.2	1.4	-4.0	1.1	-1.2	3.3	-1.1	-1.3	1.5	-1.8	-2.0
AA759519	interferon-stimulated protein (15 kDa)	1.0	-1.6	-1.2	-5.2	-1.0	-1.5	1.2	-1.2	-1.1	-1.2	-1.1	-1.2
AA750368	ribonuclease 1, pancreatic	1.7	2.3	-1.2	-5.8	-16.6	-3.3	1.8	-1.8	-4.1	-1.1	-1.2	-1.1
AA175818	interferon-induced protein with leucine-rich repeats 1	-1.1	-1.65103+	-1.2	-7.4	-1.3	-2.50237~	-1.86725+	-1.2	-1.0	-1.0	1.1	1.1
AA62109	major urinary protein 1	-1.1	-2.4	-2.67449+	-7.8	-1.1	1.43274~	-1.3	71.1	-1.8	-2.2	-1.1	-1.2

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liver	gpl	pkac	lv	stom	int	col	tr	lung	blad	kidn	plut	mam
Description	PK- AB_BONE int	PK- AB_BONE int	PK- AB_BONE int	PK- AB_BONE int	PK- AB_BONE int	PK- AB_BONE int	PK- AB_BONE int	PK- AB_BONE int	PK- AB_BONE int	PK- AB_BONE int	PK- AB_BONE int	PK- AB_BONE int
A1823752 hydroxymethylglutaryl-CoA synthase	-1.0	-1.1	3.6	-1.1	1.2	-1.2	-1.2	1.0	-1.0	-1.0	-1.1	1.2
AA746572 tyrosyl homocysteine S-methyltransferase	1.2	-1.6	3.4	-1.3	-1.6	-1.3	-1.3	-1.6	-1.5	-1.3	-1.1	-1.2
AA103346 hydroxysteroid 17-beta dehydrogenase 2	1.3698+	1.3693+	3.6	1.31794	1.0	1.41016+	1.55064+	-1.0611+	-1.0631+	1.13851+	-1.03584+	-1.13026+
AA108128 cytochrome P450, 2A4	3	-1.3	3.0	-1.3	1.4	1.0	-2.4	1.3	1.0	2.3	1.1	1.1
AA674177 cytochrome P450, 2A4	1.2	-1.6	2.8	1.1	1.3	1.7230+	-2.1	1.2	-1.0	2.1	-1.1	-1.2
AA811032 cytochrome P450, 2C7	1.0	-1.1	2.8	1.1	1.8	1.5	-1.2	-2.6	1.0	1.1	-1.1	1.6
AA107319 alcohol dehydrogenase 1, complex	1.2	-1.2	2.5	-1.4	-1.2	1.3	-1.0	-1.4	1.1	1.1	-1.3	-1.3
AA1052452 alcohol carrier, family 22 (alcohol dehydrogenase 1, family 2)	1.7	-1.3	2.6	1.0	1.0	-1.16636+	-1.7	-1.7	1.1	1.0	1.3	1.2
AA474336 symporters complex, protein 3	-2.8	1.2	2.6	1.4	1.5	2.74135+	1.1	-3.7	-2.1	-1.4	-2.3	-1.3
AA237217 protein carrier, family 2 (facilitated glucose transporter 2)	1.06901+	1.21261+	2.5	1.1	1.4	1.76237+	-2.06124+	1.20266+	1.38263+	1.0	1.33503+	1.38719+
AA638769 metallothionein 1	1.0	1.1	2.5	1.2	2.4	1.5	1.2	-1.6	-1.3	1.6	-1.9	-1.2
AA162217 pro-B-cell colony enhancing factor	1.2	-1.2	2.5	1.0	1.1	1.0	1.0	1.0	-1.1	1.0	1.0	1.0
AA274023 apoptosis inhibitor 5	1.2008+	-1.01023+	2.6	1.0683+	-1.0146+	-1.52171+	-1.07168+	1.01854+	1.07326+	1.15311+	1.35556+	1.34638+
AA643382 juvenile 1, receptor, type 1	-1.00156+	-1.22244+	2.4	1.14266+	-1.0762+	-1.37095+	1.46647+	1.34476+	1.0216+	1.0678+	1.1	-1.03468+
AA245846 hydroxysteroid dehydrogenase-2, delta-S-3-beta	1.6	-1.3	2.4	-1.2	1.2	-1.52324+	-1.5	-1.3	1.2	1.2	-1.1	1.2
AA750070 Mus musculus triacylglycerol hydrolase (HDLA) iso	1.2	-1.4	2.4	1.1	1.1	1.4	-1.1	1.2	-1.5	1.1	-1.1	-1.3
AA027607 hydroxysteroid 17-beta dehydrogenase 2	1.2667+	-1.3066+	2.4	1.3	1.6377+	-1.26025+	-1.26348+	-1.02353+	1.3	1.3	-1.2	1.2
A778916 fatty acid CoA synthase A (fatty acyl-CoA synthetase 2)	1.0	-1.4	2.4	1.0	-1.0	-1.2	-1.6	-1.2	-1.1	1.2	1.5	-1.4
A32201 p53b, nuclear	1.13857+	1.06101+	2.5	-1.16185+	1.06891+	-1.06459+	1.5232+	-1.53938+	1.1171+	1.16765+	-1.1181+	-1.1208+
A047868 RIKEN cDNA 210041F14 gene	-1.2	-1.058+	2.5	-1.1	-1.26887+	1.10688+	-1.11183+	-1.52779+	-1.12343+	-1.3	-1.3	-1.0113+
A3306693 ESTs, Weakly similar to 146271 hypothetical protein DKF5456	1.1	-1.1	2.3	1.0	-1.0	1.6534+	-1.3	1.0	-1.1	-1.1	-1.2	-1.2
64P263.1 (Hsp60)	-1.1	1.05534+	2.6	1.1	-1.2	-1.00268+	1.21671+	-1.0	1.1	-1.2	1.1	1.1
A244383 retinoic acid early transcript, genome	-1.1	-1.6	2.2	1.3	1.2	1.0	-1.1	-1.1	1.2	1.1	-1.1	-1.1
AA713955 ficolin A	1.1	-1.6	2.2	1.3	1.6	1.3414+	1.0	-2.0	-1.4	-1.3	-2.0	1.0
W05034 ESTs	-1.2	1.3	2.2	1.5	1.6	1.3414+	1.0	-2.0	-1.4	-1.3	-2.0	1.0
AA62108 ESTs, Weakly similar to COXA HUMAN, COMPLEMENT CO	2.3	-1.7	2.2	-1.0	1.1	2.5778+	-1.6	-2.2	-1.5	-1.3	-1.4	-2.7
MPONET_C3 ALPHA CHAIN PRECURSOR (Hsp60)	1.0	1.9	2.2	-1.7	1.4	-1.26007+	-1.2	1.0	-1.1	1.3	-1.4	-1.3
A117310 beta containing monooxygenase 1	1.7	1.0	2.2	-1.1	-1.3	-1.2646+	1.0	-1.1	1.2	1.1	-1.4	-1.1
A778916 hydroxysteroid 11-beta dehydrogenase 1	1.7	1.0	2.2	-1.1	-1.3	-1.2646+	1.0	-1.1	1.2	1.1	-1.4	-1.1

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TABLE 2



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AA106162 cytochrome P450, 2c26	1.0	-1.1	1.2	-1.0	1.7	-1.4	-1.7	-1.2	1.1	-1.0	-1.1
AA1597312 hydroxysteroid dehydrogenase-1, delta<-3-beta	1.2	-1.5	1.2	1.3	1.51336+	1.0	-2.52674**	-1.2	1.2	-1.5	1.1
AA261460 hypothetical protein, l84	1.2	1.1	2.7	-1.3	1.1	1.04753+	-1.0	-1.2	1.1	-1.0	-1.1
W053070 ESTs	-1.2	1.4	1.2	1.7	1.1	1.1	-2.6	-1.4	-2.3	-1.1	-2.6
W064774 metallothionein 2	-1.2	-2.2	2.1	1.2	-1.9	1.1	-1.6	-1.1	1.0	-1.9	1.0
AA680607 carnitine acetyltransferase 3	1.1	-1.3	2.1	-1.5	1.1	-2.4	-1.7	-2.1	-1.3	-1.2	-1.6
AA590948 ATP-binding cassette, sub-family A (ABC1), member 8	-1.03399+	-1.29908+	2.1	-1.07194+	1.39706+	1.0351+	-1.45781+	1.4	1.3	1.0	1.36564+
AA674302 E57A, Moderately similar to A23772, LINE-1, hypothetical protein, - mouse (Mus musculus)	-1.2	-1.5	2.1	-1.3	1.4	2.0	-1.0	-1.3	-1.3	1.2	-1.1
AA260933 peroxisomal protein, mouse 11a	1.3	1.36983+	2.1	1.4	1.3	-1.02652+	-1.0677+	-1.5	1.1	1.7	1.2
AA271463 E37C, Weakly similar to related short-chain dehydrogenase/reductase, mSDP1 (Mus musculus)	1.7	1.6	2.1	1.1	-1.2	2.03505+	-1.5	-2.1	1.2	-1.2	1.0
AA108741 RIKEN cDNA 081002519, gene	1.1	1.0	2.1	-1.3	1.3	1.0	1.2	1.2	1.1	1.1	1.0
AA572640 RIKEN cDNA 1700124702, gene	-1.10123+	-1.00384+	2.1	-1.2	1.2	1.18494+	-1.26090+	-1.9	-1.0	-1.2	-1.2
AA471008 3-hydroxy-5-methylglutaryl-CoA synthase A, rat	-1.1	-1.6	2.0	1.3	-1.5	-2.18933+	-1.1	-1.3	-1.0	1.3	-1.2
AA272831 bovine homocysteine methyltransferase	1.3	-1.3	2.0	-1.0	1.1	-1.62406+	-1.1	-4.7	1.3	-1.3	-1.1
AA580508 serum albumin, variant	2.0	-1.7	2.0	-1.1	-1.1	1.16346+	-1.3	-2.1	-1.4	-1.5	-1.3
W18463, thioester S-methyltransferase	1.0	-1.5	2.0	1.3	-1.6	-1.6	-1.9	-1.0	-1.7	1.2	-1.0
AA487821 S-phase kinase-associated protein 2 (p45)	-1.8	-1.2	2.1	1.5	1.2	2.17571+	-1.73102+	-2.2	-1.6	-1.4	-1.8
AA587403 glycine N-methyltransferase	1.1	1.2	2.0	1.1	1.3	1.37381+	-1.0	-1.4	-1.1	1.0	1.2
AA420359 DNA segment, Chr. 6, SPATO Doi U9, secreted	1.1	1.1	2.0	1.5	-1.3	-1.1	1.1	1.3	1.0	1.1	-1.1
AA116636 RIKEN cDNA 1110013405, gene	-1.5	-1.0	2.0	1.4	1.2	2.10442+	-1.2	-1.6	-1.3	-1.3	-1.6
AA511066 glutathione S-transferase, theta 2	1.4	1.2	2.0	-1.1	-1.1	1.0	-1.4	-1.3	1.2	1.0	1.1
AA024217 public domain EST	-2.5	1.6	2.0	1.2	2.3	2.7	-1.0	-4.2	-4.9	-1.2	-2.3
AA95530 cytochrome P450, 2b13, phenanthrene inducible, type c	1.4	-1.1	2.0	1.0	2.0	2.03014+	1.0	1.1	1.2	-1.2	1.1
AA415254 glutamate malate dehydrogenase 1, soluble	1.3	1.1	2.0	-1.1	1.5	1.0	1.1	1.0	1.2	1.4	1.4
AA237607 pyruvate kinase liver and red blood cell	-1.4	-1.2	1.9	-1.2	1.5	1.3	-2.3	-1.2	-1.1	1.0	1.1
AA422117 UDP-glucuronosyltransferase 1 family, member 1	-1.0	-1.4	1.9	-1.4	1.1	1.5	-1.3	-1.2	1.1	-1.2	-1.1
W77426 selenium binding protein 1	1.0	-1.4	1.5	1.4	1.1	-1.8	-1.4	-1.2	-1.0	1.1	-1.1
LINE KNA056 (HsJens16)	1.4	-1.0	1.9	-1.3	1.2	1.0904+	-1.3	-1.1	1.2	1.2	-1.1
AA62274 arabin N-sulfotransferase	-1.0	-1.2	1.7	1.4	-1.6	1.20148+	-1.0	-1.4	-1.1	-1.2	-1.4
AA077663 RIKEN cDNA 2310057716, gene	-1.2	1.2	1.5	1.1	1.2	1.59785+	1.5	1.1	1.1	-1.4	-1.6
AA343705 RIKEN cDNA 2410012702, gene	-1.2	-1.0	1.5	1.1	-1.4	1.19407+	-1.4	-1.4	-1.2	-1.1	-1.2
AA515558 urate oxidase	1.51631+	-1.05014+	2.1	1.3	1.6068+	1.10047+	-1.3	-2.5066+	1.02179+	-1.2	1.3
AA422002 cytochrome P450, 2c40	1.3	-1.2	1.5	1.3	1.4	1.4	1.1	-3.9	-1.1	-1.2	-1.3
AA671461 RIKEN cDNA 1110007705, gene	1.3	1.4653+	1.7	-1.3	1.4	-1.15618+	1.03774+	1.1	1.1	-1.0	-1.1

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TABLE 2

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A455954 cytochrome P450_2b6 phenobarbital inducible, clone 8	-1.1	-1.4	1.1	1.3	2.4	3.8	-1.3	1.1	1.3	1.2	1.1	1.2
A454941 myosin heavy chain 11, isoform 1, alpha 1	1.2	-1.2	1.1	1.2	-1.1	1.2471-	-2.2	-1.1	1.3	1.0	-1.1	1.1
6.5 clone MGC-7544 mRNA, complete cds	-1.2	1.0	1.3	1.1	1.2	1.05614-	-1.1126+	-1.1	-1.1	-1.1	-1.1	-1.2
A260296 retenease 31	1.2	-1.01004+	1.1	1.2	1.1	-1.29474-	-1.14539+	-1.6571+	-1.2	-1.0	1.1	1.6
A172093 alpha-helical factor 4	1.1	-1.01893+	1.0	1.2	1.2	-2.41321-	1.23402+	-1.1	1.2	1.2	-1.1	1.1
A128554 aldo-keto reductase family 1, member C1	-1.0	1.0	1.1	1.8	1.1	1.14181-	-1.7	1.5	1.0	1.2	1.5	1.8
A4081722 leucine complex 1, acidic gene 13	1.2	-1.7	-1.9	1.1	1.2	1.23314-	-1.7	1.5	-1.1	-1.4	1.5	1.5
A028346 insulin complex 1, acidic gene 19	-1.4	-1.6	-1.9	-1.5	1.0	-1.2	-2.3	1.1	-1.1	-1.3	-1.2	-1.2
A4003337 RIKEN cDNA 290005D14, clone	-1.4	-1.1	-1.9	-1.2	1.1	-1.45308-	-1.0	-1.2	-1.2	-1.2	-1.2	-1.1
A1390445 ESTs	1.1	-1.61106+	-1.9	-1.6	-1.4	-1.16439-	-1.06446+	-1.0	-1.1	-1.2	-1.1	-1.1
A4671784 Mus musculus mmp protein (Mmp) gene, complete cds	-1.6	-1.9	-1.9	-2.2	-1.0	-1.1	-1.2	-1.4	-1.6	-1.6	-1.6	-1.6
N33904 proopiomelanocortin, type VI, alpha 2	-1.1	-1.3	-1.9	1.5	-1.0	1.0	-1.4	-1.1	1.3	-1.3	-1.3	-1.5
A4407019 ESTs	-1.1	1.0	-1.9	1.6	1.3	-1.0662-	-1.0	1.2	-1.0	1.1	1.1	1.4
N62007 neuron specific gene family member 2	-1.5	-1.5	-1.9	-2.3	-1.3	-1.0	1.4	-2.0	-1.6	-1.4	-1.3	-1.5
A4794055 cytochrome c b1 protein	1.0	1.4	-1.9	-1.3	1.7	-2.0	-1.3	-1.0	-1.4	-1.0	-1.3	1.1
A183151 heparan sulfate 2-O-sulfotransferase 1	-1.2	-1.0	-1.9	1.4	1.3	-1.34248-	-1.0	1.2	-1.1	-1.1	1.0	-1.1
A4273420 scytinin 1	-1.3	-1.5	-1.9	-1.7	-1.1	-1.47838-	-1.11692+	-1.0	-1.4	-1.1	-1.3	-1.0
A4619402 paracatalin-associated protein	1.7	19.5	-1.9	1.2	1.1	-2.4	-1.1	-1.3	1.0	-1.2	1.3	1.1
A4617162 RIKEN cDNA 493405E14, clone	-1.3	1.1	-1.9	-1.4	1.3	-1.81988-	1.5	-1.0	-1.0	-1.0	-1.0	-1.1
A191831 ESTs	-1.5	-1.4	-2.0	-1.6	-1.1	1.6229-	1.37023+	-1.3	-1.2	-1.3	-1.5	-1.5
A192552 chorbyl-12-methylate-13-acetate-inducible protein 1	-1.3	-1.3	-2.0	-1.6	-1.2	-1.25042-	-1.0	-1.1	-1.2	-1.4	-1.2	-1.1
A4671205 public domain EST	1.3	-1.4	-2.0	1.4	-1.7	-3.0	-3.1	-1.3	1.2	1.3	1.4	-1.7
A4446867 RIKEN cDNA 483241C03, clone	1.3	-1.2	-2.0	2.1	-1.0	1.1	1.3	-1.2	1.9	1.4	1.8	1.9
A4691215 myo acid binding protein 5, epididymal	1.2	-1.2	-2.0	-1.0	1.2	5.44959-	1.1	1.1	1.3	1.1	-1.1	-1.3
A464243 CD68-like cytosolic strand	-1.4	-1.0	-2.0	-1.7	1.1	-2.0	1.2	-1.2	-1.2	-1.1	-1.2	-1.2
N92553 insulin-like growth factor binding protein 5	-1.0	-1.3	-2.0	1.2	1.4	1.14404-	1.1	1.0	-1.0	1.1	1.0	-1.8
A4412831 Mus musculus clone MGC-8604, mRNA, complete cds	-1.2	-1.2	-2.1	-1.1	1.0	1.07343-	-1.0	-1.1	-1.1	-1.1	-1.1	-1.1
A4728855 RIKEN cDNA 3294029Z2, clone	1.3	1.5	-2.1	-1.5	-1.7	-1.4	-1.4	-1.2	1.4	1.2	1.1	-1.3
A1045940 clathrin 4	-1.6	1.5	-2.1	-1.8	1.7	-2.7	1.5	-1.1	-1.2	-1.3	-1.2	-1.2
A4482626 ESTs	-1.4	1.1	-2.1	-1.8	1.3	-3.0	-1.2	-1.2	-1.2	-1.3	1.0	-1.2
A4884403 ESTs	-1.4	1.7	-2.3	-2.0	2.0	-2.4	1.5	-1.0	-1.3	-1.3	-1.1	-1.1
A4450922 test stock 700d protein 5, (glucose-regulated protein 78kd)	1.1	1.6	2.4	2.2	2.4	-1.6	1.6	-1.3	1.2	-1.1	-1.1	-1.2

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TABLE 2

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pancreas	spl	panc	liv	stom	int	col	br	lung	blad	kidn	pilot	mam
	Re_Bioener	Re_Bioener	Re_Bioener	Re_Bioener	Re_Bioener	Re_Bioener	Re_Bioener	Re_Bioener	Re_Bioener	Re_Bioener	Re_Bioener	Re_Bioener
Description												
AA515407 pancreatic-actin-associated protein	1.7	18.5	-1.9	1.2	4.7	-2.4	-4.1	-1.3	1.0	-1.2	1.3	1.1
AA520401 TATA box binding protein (TBP)	1.2	3.4	1.1	-1.5	-1.8	1.4	1.4	-1.4	1.1	1.1	-1.6	1.2
AA520402 TATA box binding protein (TBP)	1.1	3.0	1.2	-2.0	-1.8	-4.4	1.3	-1.1	1.1	1.4	-1.2	1.2
AA520403 TBP-associated factor 1 (TAF11)	1.2	2.4	1.2	1.1	1.4	-3.3	1.1	-1.2	-1.3	1.1	-1.1	1.1
AA520404 TBP-associated factor 2 (TAF2)	1.7	2.3	-1.2	-5.8	-16.6	-3.3	1.8	-1.9	-4.1	-1.1	-1.2	-1.1
AA570389 RNA polymerase II, subunit 1	-1.4	3.2	1.0	-1.3	-2.1	1.3	-1.6	-1.5	-1.1	-1.2	-1.3	-1.1
AA570390 RNA polymerase II, subunit 2	-1.1	2.2	-1.1	1.1	1.1	-1.6	1.3	-1.4	-1.3	1.0	-1.2	-1.1
AA570391 RNA polymerase II, subunit 3	1.4	2.1	1.0	1.4	1.2	-1.0	1.0	1.5	1.3	1.4	1.3	1.2
AA570392 RNA polymerase II, subunit 4	1.4	2.0	1.1	-1.2	-1.0	-1.2	-1.1	-1.2	1.1	1.1	-1.1	1.1
AA570393 RNA polymerase II, subunit 5	1.1	2.0	-1.2	1.8	1.4	1.00011+	1.4	1.5	1.3	1.3	1.3	1.5
AA570394 RNA polymerase II, subunit 6	1.4	2.0	1.0	1.3	1.2	-1.0	1.1	1.4	1.4	1.2	1.4	1.4
AA570395 RNA polymerase II, subunit 7	1.4	2.0	1.0	1.3	1.2	-1.1	1.2	1.3	1.2	1.3	1.4	1.3
AA570396 RNA polymerase II, subunit 8	-1.0	2.0	1.1	-1.9	1.1	-1.2	1.2	1.0	1.1	1.4	1.0	-1.0
AA570397 RNA polymerase II, subunit 9	1.3	1.9	-1.2	-1.2	1.1	-1.7	1.2	-1.2	1.1	1.0	-1.2	1.0
AA570398 RNA polymerase II, subunit 10	1.7	1.6	-1.4	3.1	2.0	1.31548+	1.3	2.3	2.0	1.6	2.2	2.1
AA570399 RNA polymerase II, subunit 11	1.2	1.6	-1.2	-1.1	-1.0	-1.8	1.3	-1.1	1.0	1.1	-1.2	1.0
AA570400 RNA polymerase II, subunit 12	1.2	1.6	-1.1	-1.1	-1.1	-1.1	1.1	-1.2	-1.0	-1.1	-1.2	-1.2
AA570401 RNA polymerase II, subunit 13	1.6	1.5	-1.3	3.6	1.6	-1.01509+	1.1	2.2	2.1	1.6	2.5	2.3
AA570402 RNA polymerase II, subunit 14	1.4	1.6	1.0	1.5	1.2	1.1	1.2	1.4	1.5	1.2	1.4	1.3
AA570403 RNA polymerase II, subunit 15	1.3	1.8	1.1	2.1	1.5	1.20006+	1.7	1.4	1.5	1.5	1.5	1.4
AA570404 RNA polymerase II, subunit 16	1.3	1.8	1.1	-1.0	-1.6	1.2	1.2	-1.0	1.2	-1.9	1.0	-1.3
AA570405 RNA polymerase II, subunit 17	1.23774+	1.8	-1.3504+	2.4	1.6	1.1554+	1.432+	1.5	1.2	1.4	1.4	1.1
AA570406 RNA polymerase II, subunit 18	-1.7	-1.9	-1.3	-2.2	-1.2	-1.0	-1.3	-1.4	-1.5	-1.2	-1.4	-1.5
AA570407 RNA polymerase II, subunit 19	1.7	-1.9	1.0	-1.2	-1.1	-1.24501+	-1.2	-1.2	-1.1	-1.4	-1.1	1.2
AA570408 RNA polymerase II, subunit 20	-1.0	-1.9	-1.3	-1.1	-1.5	1.2	1.13857+	1.3	-1.1	-1.2	1.2	-1.1
AA570409 RNA polymerase II, subunit 21	-1.0	-1.9	-1.2	-1.3	-1.1	1.31076+	-1.8	-1.3	-1.6	1.0	1.1	-1.4
AA570410 RNA polymerase II, subunit 22	-1.1	-1.9	-1.2	-1.4	-1.3	1.13334+	-1.0	-1.8	-1.3	1.1	1.1	1.0
AA570411 RNA polymerase II, subunit 23	-1.6	-1.9	-1.1	-2.2	-1.0	-1.1	-1.2	-1.4	-1.6	-1.6	-1.6	-1.6
AA570412 RNA polymerase II, subunit 24	-1.1	-1.9	1.4	-1.2	-1.0	-1.15904+	1.1	1.0	-1.1	-1.2	-1.1	-1.0
AA570413 RNA polymerase II, subunit 25	1.1	-1.9	-1.1	-1.1	-1.7	1.1	1.0	1.2	-1.1	-1.2	1.1	-1.1
AA570414 RNA polymerase II, subunit 26	-1.8	-1.9	-1.5	-1.8	-1.0	-1.6878+	-1.1	-1.2	-1.4	-1.2	-1.3	-1.5

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TABLE 2

PANCREAS

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A472330 ESTs	-1.4	-1.8	-1.1	-1.3	-1.8	1.0	-1.1	-1.1	-1.3	-1.1	-1.0
A400322 peroxisomal fatty-acyl protein	-1.4	-1.9	-1.3	-2.1	-1.0	-1.1	-1.2	-1.2	-1.4	-1.0	-1.2
W06636 carnitine lipase 2	-1.5	-1.9	-1.4	1.4	1.0	1.3	-2.3	-1.1	1.0	1.2	1.1
A065699 ESTs	-1.5	-1.9	-1.5	-1.8	-1.3	-1.43333~	-1.00226~	-1.1	-1.6	-1.4	-1.2
A117210 favin oxidoreductase 1	1.0	-1.9	-2.3	-1.7	-1.4	-1.20007~	-1.2	1.0	-1.1	1.3	-1.3
A123207 ATPase, Cu++ transporter, beta polypeptide	1.2	-1.9	1.2	-1.4	-1.0	1.17934~	-1.2	-21.9	-1.5	-1.8	-1.7
A479591 ESTs. Weakly similar to A48441_Mouse_18.5_mRNA_complete cds + mouse [H. musculus]	-1.1	-1.9	-1.3	1.0	1.2	-1.2	-1.3	1.1	-1.1	1.1	1.0
A065173 ESTs	-1.5	-1.9	-1.4	-1.6	-1.4	-1.48844~	-1.7	-1.5	-1.7	-1.3	-1.4
A468426 ESTs	1.0	-1.9	-1.2	1.1	-1.8	1.0	1.2	1.1	-1.1	-1.3	1.2
A403870 keratin complex 2, basic, gene 4	1.2	-1.9	-1.3	-1.0	-1.0	1.44871~	-2.1	1.6	-1.4	-1.1	1.5
W15822 keratin complex 2, basic, gene 4	1.2	-2.0	-1.3	-1.1	1.9	1.65222~	-1.3	-1.7	1.3	-1.1	-1.3
A135332 transaminase 3, E polypeptide	-2.0	-2.0	-1.4	-2.3	-1.2	-1.2	-1.2	-1.2	-1.7	-1.4	-1.7
A172721_1 rat_musculus_11_100_nucleotide_protein_precursor_mRNA_co cds + rat [R. norvegicus]	1.1	-2.0	-1.4	1.7	1.5	2.4	-1.6	1.2	1.1	1.1	1.5
A120024 trophoblast specific protein	1.5	-2.0	-1.2	1.5	1.1	-1.0	-2.2	-1.2	1.4	1.1	1.2
A408168 uromodulin	-1.2	-2.0	-1.0	1.1	-1.3	1.0	-1.0	-1.4	-1.7	1.1	-1.2
A4823704 Public domain EST	1.2	-2.0	-1.0	-1.0	-1.7	1.2	-1.0	1.3	-1.0	-1.2	1.2
A4726182 keratin complex 1, acidic, gene 16	-1.1	-2.0	1.2	-1.1	-1.0	1.3	-1.5	-1.2	1.3	-1.2	-1.1
A054842 foetal actinin 2	-2.1	-2.0	-1.4	-2.2	-1.2	-1.1	-1.3	-1.4	-1.4	-1.4	-1.5
W53106_ELAN embryonic lethal abnormal vision_Drosophila> like 3 (H. sapiens C)	-1.5	-2.0	-1.7	-1.8	-1.2	-1.48007~	1.0	-1.2	-1.6	-1.3	-1.3
A4481911 Mas musculus, clone MGC87277_mRNA_complete cds	-1.1	-2.0	-1.8	1.0	-1.8	-2.3	-1.5	-2.4	-1.4	-1.4	-1.4
A4784176 ESTs. Moderately similar to SP4-1, line protein p.234. (R. norvegicus)	-1.0	-2.0	-1.2	-1.2	-2.0	1.2	1.2	1.3	-1.3	1.1	-1.1
A477068 poliovirus material 1	1.4	-2.0	1.0	1.1	-1.8	1.2	1.3	1.3	1.0	-1.3	1.4
A4883177 ESTs	-1.9	-2.1	-1.6	-2.3	-1.1	-1.2	-1.0	-1.5	-1.6	-1.6	-1.6
A4727827 ankyrin 1, cytosolic	-1.8	-2.1	-1.8	-2.5	-1.3	-1.2	-1.4	-1.4	-1.6	-1.6	-1.7
A4717019 ATPase, Cu++ transporter, cardiac muscle, fetal, with 1	-1.2	-2.1	-1.1	-1.5	-1.3	1.2	-2.8	-1.4	-1.8	-1.2	1.1
A484151 CDC-like kinase	1.5	-2.1	-1.3	1.1	-2.0	1.4	-1.3	1.0	1.4	-2.1	1.1
W54403 ATPase, Cu++ transporter, beta polypeptide	1.2	-2.1	1.1	-1.0	1.2	1.3	-2.9	-1.9	1.1	-1.1	1.2
A2434952 cytochrome b5 (cytochrome b5 reductase)	-1.1	-2.1	-1.7	-1.8	-1.2	-1.34929~	-1.2	1.1	-1.0	-1.3	-1.1
A1305457 redox binding protein 2, cellular	-2.0	-2.1	-1.6	-1.9	1.5	1.6	-1.3	-1.9	-1.6	-1.9	-1.5
A4732746 ESTs	-2.0	-2.2	-1.6	-2.9	-1.3	-1.2	-1.6	-1.7	-1.8	-1.7	-1.8
A4136265 RIKEN cDNA 201030G21 gene	-1.1	-2.2	-1.5	-1.2	-1.0	-1.9	-1.1	1.1	-1.3	-1.0	-2.4
W56474 metallothionein 2	1.2	-2.2	-1.3	1.1	-2.2	1.1	-1.0	1.3	-1.3	-1.4	1.2
A4414790 leukotriene A4 hydrolase	-2.1	-2.2	-1.6	-2.8	-1.3	-1.8	-1.2	-1.7	-2.0	-1.7	-1.8
A4186126 tumor necrosis factor receptor superfamily, member 9	1.3	-2.3	-1.1	-1.3	-1.3	1.2	-2.7	-1.3	-1.1	-1.2	1.1

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AA022105 major urinary protein 1	-1.1	-2.4	-26.76497	-7.8	-1.1	1.82224	-1.3	-71.1	-1.8	-2.2	-1.1	-1.2
AA021997 myoglobin	-1.0	-2.5	1.0	1.1	1.0	1.2	-1.8	-1.7	-4.3	22.3	-1.1	-1.7
AA022267 myosin light chain, alkali, fast skeletal muscle	1.4	-2.5	-1.2	-1.1	-1.1	1.97855	-1.3	1.0	-1.8	-1.4	-1.2	-1.6
AA007671 interstitial A, peridex	1.9	-3.1	-1.1	1.1	-1.4	2.08884	-1.2	1.4	1.1	-1.7	1.5	1.3
AA444634 ESTs, Weakly similar to MDPT_MOUSE, MICROSONAL DIPE	-2.1	-3.9	1.2	-1.4	-1.1	-1.19880	-1.5	1.0	1.3	-1.3	-1.3	1.3
PTDASE PRECURSOR (M.muscle/lal)	-1.2	-5.8	1.1	-1.8	1.1	-1.0	-1.0	-1.1	1.5	-1.3	-1.1	-1.1
W04282 heat shock protein, 25 kDa	-1.2	-5.8	1.1	-1.8	1.1	-1.0	-1.0	-1.1	1.5	-1.3	-1.1	-1.1
AS90136, RIKEN cDNA 393401B19, gene	-1.4	-10.7	-1.1	-5.0	-1.2	-5.1	-1.3	-1.2	1.5	-1.9	-1.3	-1.1

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AA01602 Insulin antigen 2	-2.1	-2.0	-1.4	-2.2	-1.2	-1.1	-1.3	-1.4	-1.4	-1.4	-1.4	-1.5
AA41790 leukotriene A4 hydrolase	-2.1	-2.2	-1.6	-2.8	-1.3	-1.6	-1.2	-1.7	-2.0	-1.7	-1.6	-1.8
AA014727 tumor-suppressing subchromosomal transferable fragment 3	-2.1	1.1	1.3	-1.2	1.1	2.6534E-18	-1.8	-3.0	-2.1	-1.8	-2.9	-1.0
AA46646 cell division cycle 2 homolog (S. pombe) like 2	-2.1	-1.1	1.3	1.4	1.1	2.3	-1.5	-3.0	-2.3	-1.5	-2.4	-1.4
AA44468 ESTs, Weakly similar to MGP1_MOUSE_MGROSOMAL_DIREP	-2.1	-3.9	1.2	-1.4	-1.1	-1.18889E-18	1.8	1.0	1.3	-1.3	-1.3	1.3
TIDASE PRECURSOR [Musculus]	-2.1	-3.9	1.2	-1.4	-1.1	-1.18889E-18	1.8	1.0	1.3	-1.3	-1.3	1.3
AA09466 ESTs	-2.2	-1.2	1.4	1.1	-1.2	1.17951E-11	1.0	-1.2	-1.1	-1.2	-1.2	1.4
AS02937 calbindin-D9K	-2.2	-1.3	1.2	1.5	-3.5	-4.1	1.0	-1.2	-1.1	-1.2	-1.2	1.4
AA037183 tropotin 2	-2.2	-1.7	-1.8	-1.3	-1.2	-1.0	-1.4	-1.1	1.2	-2.02982E-16	1.1	1.1
AA034678 rhodopsin	-2.3	1.0	1.2	-1.0	1.2	2.4	-1.3	-2.5	-2.1	-1.4	-2.6	-1.4
AA414853 ESTs, Weakly similar to KIAA0542 protein (H. sapiens)	-2.4	-1.13914E-11	-1.5	1.1	-1.2	1.26167E-20	1.7853E-12	-1.27379E-13	-1.1	-1.1	-1.26951E-11	-1.1
AA717229 ESTs, Weakly similar to zinc finger protein 85 [M.musculus]	-2.4	1.2	1.3	1.2	1.2	1.7415E-20	-2.0	-3.9	-2.2	-1.4	-2.4	-1.4
AA92161 proteinase 3	-2.4	1.1	1.2	-1.1	1.1	1.44238E-11	-1.3706E-14	-1.2	-1.2	-1.2	-1.1	1.1
AA178946 forkhead box C2	-2.5	1.1	1.4	1.4	1.1	1.7	-1.7	-3.0	-2.3	-1.8	-2.5	-1.1
AA024177 PstIIc domain EST	-2.5	1.8	2.0	1.2	2.3	2.2	-1.0	-4.2	-1.9	-1.2	-2.3	1.1
AA02651 ESTs	-2.6	-1.1	1.0	-1.4	1.2	1.2	-1.6	-2.6	-2.1	-1.7	-2.2	-1.5
AA474101 tumor-associated calcium signal transducer 2	-2.6	-1.1	1.5	1.3	1.2	8.559E-17	-2.1	-1.5	-1.5	-1.5	-2.4	-1.2
AA474533 synaptosomal complex protein 3	-2.8	1.2	2.6	1.4	1.6	2.7413E-11	-3.7	-2.1	-1.4	-2.3	-1.3	-1.3
AA031515 myeloperoxidase	-2.9	-1.1	1.0	-1.1	1.6	1.05319E-13	1.0	-1.3	-1.9	-1.9	1.0	1.1
AA183268 ESTs	-3.2	1.4	1.5	1.5	1.3	1.7	-1.3	-5.6	-3.0	-1.8	-3.9	-1.4
AA026282 neurophilic granule protein	-4.0	1.32257E-12	1.2	-1.0	1.26109E-11	-1.34714E-11	1.7277E-15	1.5	1.2	-1.1	1.0	-1.4

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TABLE 3





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Description	ID	spl	panc	liver	stom	intest	colon	brain	lung	blad	kidney	plut	Breast	Remarks
AA242102 villin	MG225.GS.A- G.0217AAQJF8													a specific marker expressed in tumors of the digestive tract, renal proximal tubules, and hepatic bile duct. PMID: 11717541
A104552 lactate dehydrogenase 3, C chain, sperm specific	MG225.GS.A- G.0217AARBE3													Expressed in many cancers PMID: 12433276
A1329499 epidermal growth factor	MG225.GS.A- G.0217AAR3H3													2.3 EQF, to review PMID: 1242312
AA486630 choline kinase	MG225.GS.A- G.021DAQJF5													Elevated in breast, lung, colorectal, and prostate tumors. PMID: 12175620
W14224 N-myc downstream regulated 1	MG225.GS.A- G.021DAARB11													Overexpressed in skin hyperplasia, PMID: 11748622, p53 responsive gene?, androgen dependent gene
AA270885 parvalbumin	MG225.GS.A- G.0218AAR4C9													Marker of specific tumors, (like chromophobe renal carcinoma, PMID: 11504835) by expression on specific parental cell types, Neuroendocrine marker (PMID: 12792676)
AA760002 beta-glucuronidase structural, beta-glucuronidase precursor	MG225.GS.A- G.021WAP4G5													Elevation in poor differentiation colorectal tumor. PMID: 11717961, in pancreatic cancer PMID: 10361372, -1.1
W16059 glutathione S-transferase omega 1	MG225.GS.A- G.0217AARBC8													upregulated in invasive human breast cancer lines, PMID: 12091914

Table 4

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AA25345 hydroxysteroid 17-beta dehydrogenase 9	MG225.GS.A- G.021HAQ1C2					1,41016 1.0	1,5526 4++	1,106 11+	1,0531 +	1,1385 1+	1,0539- 9+	1,13526+	Expression elevated in epithelial ovarian tumors PMID: 8729877
AA027607 hydroxysteroid 17-beta dehydrogenase 2	MG225.GS.A- G.021UAR2X2					1,31173 3.0+							Inversed correlation with breast cancer progression PMID: 11731426 (type II decrease and type I increase high risk)
						1,58774 1.3		1,2834 8+	1,023 58+	1.3	1.3	1.2	clusterin is a marker of anaplastic large cell lymphoma PMID: 12429902 expressed in human pancreatic cancer PMID: 12370533, breast carcinoma PMID: 10934144
AA210461 clusterin	MG225.GS.A- G.021TAQ0A1												
AA790388 ribonuclease pancreatic	MG225.GS.A- G.021PAAGQC11												Expression elevated in pancreatic adenocarcinoma and pancreatic isletoma PMID: 11002220

Table 4

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Prostate	Fold	Fold	Relation to cancer
AA92642 melanoma-inhibitory-activity protein, cartilage derived retinoic acid sensitive protein (Cdrap), (MIA/CD-RAP)	2.5		correlate with the progression of malignant melanoma and chondrosarcoma, PMID: 11916321
AA107101 prostate stem cell antigen, PSCA	2		overexpressed in human prostate cancers, PMID: 12172427
AI853055 Cystatin E (cystatin M)		4.7	Expressed in neoplastic epidermis PMID: 12100189
M31885 inhibitor of DNA binding 1, DNA-binding protein inhibitor ID-1			Expression elevated in nasopharyngeal carcinoma cells PMID: 12203366, Overexpressed in prostate cancer
AW12874 PCNA		5.1	PMID: 11992094, overexpressed in medullary thyroid cancer PMID: 1111462
apolipoprotein D		3.2	Well known
Secretory leukoprotease inhibitor gene	3	2	Prostate tumor marker 9549289
glutathione peroxidase 3 (plasma)		7	Ovarian cancer candidate marker 11358798
apolipoprotein E	12	2.5	Ovarian cancer candidate marker 11358798
prostaglandin D2 synthase (21kD, brain)	25	25	Ovarian cancer candidate marker 11358798
glutaryl aminopeptidase	12	14	Meningioma marker 11266526
carbonic anhydrase VI	28	5.2	Elevated in var. cervical tumors 10838501
	5.6	2.6	Target for anti-cancer treatment 11310605

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147	AA59725	membrane protein, multidomain	Human sapiens guanine nucleotide-binding protein (G protein), type 11 (Gq class) (GNAT11), mRNA	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600	601	602	603	604	605	606	607	608	609	610	611	612	613	614	615	616	617	618	619	620	621	622	623	624	625	626	627	628	629	630	631	632	633	634	635	636	637	638	639	640	641	642	643	644	645	646	647	648	649	650	651	652	653	654	655	656	657	658	659	660	661	662	663	664	665	666	667	668	669	670	671	672	673	674	675	676	677	678	679	680	681	682	683	684	685	686	687	688	689	690	691	692	693	694	695	696	697	698	699	700	701	702	703	704	705	706	707	708	709	710	711	712	713	714	715	716	717	718	719	720	721	722	723	724	725	726	727	728	729	730	731	732	733	734	735	736	737	738	739	740	741	742	743	744	745	746	747	748	749	750	751	752	753	754	755	756	757	758	759	760	761	762	763	764	765	766	767	768	769	770	771	772	773	774	775	776	777	778	779	780	781	782	783	784	785	786	787	788	789	790	791	792	793	794	795	796	797	798	799	800	801	802	803	804	805	806	807	808	809	810	811	812	813	814	815	816	817	818	819	820	821	822	823	824	825	826	827	828	829	830	831	832	833	834	835	836	837	838	839	840	841	842	843	844	845	846	847	848	849	850	851	852	853	854	855	856	857	858	859	860	861	862	863	864	865	866	867	868	869	870	871	872	873	874	875	876	877	878	879	880	881	882	883	884	885	886	887	888	889	890	891	892	893	894	895	896	897	898	899	900	901	902	903	904	905	906	907	908	909	910	911	912	913	914	915	916	917	918	919	920	921	922	923	924	925	926	927	928	929	930	931	932	933	934	935	936	937	938	939	940	941	942	943	944	945	946	947	948	949	950	951	952	953	954	955	956	957	958	959	960	961	962	963	964	965	966	967	968	969	970	971	972	973	974	975	976	977	978	979	980	981	982	983	984	985	986	987	988	989	990	991	992	993	994	995	996	997	998	999	1000
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57	215	AY59304.1 ESTs	Ortho sapiens cDNA clone IMAGE:172203 F; cDNA sequence of the human gene for the protein p115 (HSP70) (HSP70), mRNA, acc. # AF033337 (HSP70), mRNA, acc. # AF033337	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
58	22	AA06225 cdc25a2.1 P. phara. 1	Homo sapiens cdc25a2.1 P. phara. 1 (HSP70), mRNA, acc. # AF033337 (HSP70), mRNA, acc. # AF033337	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
59	22	AY59304.1 ESTs	Ortho sapiens cDNA clone IMAGE:172203 F; cDNA sequence of the human gene for the protein p115 (HSP70) (HSP70), mRNA, acc. # AF033337 (HSP70), mRNA, acc. # AF033337	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
60	22	AA06225 cdc25a2.1 P. phara. 1	Homo sapiens cdc25a2.1 P. phara. 1 (HSP70), mRNA, acc. # AF033337 (HSP70), mRNA, acc. # AF033337	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
61	22	AY59304.1 ESTs	Ortho sapiens cDNA clone IMAGE:172203 F; cDNA sequence of the human gene for the protein p115 (HSP70) (HSP70), mRNA, acc. # AF033337 (HSP70), mRNA, acc. # AF033337	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
62	22	AA06225 cdc25a2.1 P. phara. 1	Homo sapiens cdc25a2.1 P. phara. 1 (HSP70), mRNA, acc. # AF03333																																																																																																				

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WO 03/058201

PCT/US02/41825

120	15	AA115597 ESTs	Human vesicular transport protein, pI 110.563 [Human, Ensembl, 201102.3657.C1]	strand: bladder	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
121	1	AA115521 Public domain EST	orthologous to Human vesicular transport protein, pI 110.563 [Human, Ensembl, 201102.3657.C1]	strand: bladder	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
122	14	AA118468 ESTs	orthologous to Human vesicular transport protein, pI 110.563 [Human, Ensembl, 201102.3657.C1]	strand: bladder	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
123	12	AA045497 ESTs	orthologous to Human vesicular transport protein, pI 110.563 [Human, Ensembl, 201102.3657.C1]	strand: bladder	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
124	31	AA412921 EGEN GENA_4201142D gene	orthologous to Human vesicular transport protein, pI 110.563 [Human, Ensembl, 201102.3657.C1]	strand: bladder	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
125	14	AA073926 ESTs	orthologous to Human vesicular transport protein, pI 110.563 [Human, Ensembl, 201102.3657.C1]	strand: bladder	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
126	45	AA412879 EGEN GENA_C3000039 gene	orthologous to Human vesicular transport protein, pI 110.563 [Human, Ensembl, 201102.3657.C1]	strand: bladder	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
127	6	AA481983 EST	orthologous to Human vesicular transport protein, pI 110.563 [Human, Ensembl, 201102.3657.C1]	strand: bladder	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
128	7	AA623175 ESTs	orthologous to Human vesicular transport protein, pI 110.563 [Human, Ensembl, 201102.3657.C1]	strand: bladder	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30

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TABLE 5 (Contd.)

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344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600	601	602	603	604	605	606	607	608	609	610	611	612	613	614	615	616	617	618	619	620	621	622	623	624	625	626	627	628	629	630	631	632	633	634	635	636	637	638	639	640	641	642	643	644	645	646	647	648	649	650	651	652	653	654	655	656	657	658	659	660	661	662	663	664	665	666	667	668	669	670	671	672	673	674	675	676	677	678	679	680	681	682	683	684	685	686	687	688	689	690	691	692	693	694	695	696	697	698	699	700	701	702	703	704	705	706	707	708	709	710	711	712	713	714	715	716	717	718	719	720	721	722	723	724	725	726	727	728	729	730	731	732	733	734	735	736	737	738	739	740	741	742	743	744	745	746	747	748	749	750	751	752	753	754	755	756	757	758	759	760	761	762	763	764	765	766	767	768	769	770	771	772	773	774	775	776	777	778	779	780	781	782	783	784	785	786	787	788	789	790	791	792	793	794	795	796	797	798	799	800	801	802	803	804	805	806	807	808	809	810	811	812	813	814	815	816	817	818	819	820	821	822	823	824	825	826	827	828	829	830	831	832	833	834	835	836	837	838	839	840	841	842	843	844	845	846	847	848	849	850	851	852	853	854
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34	14	AI550591_RIKEN_cDNA_2010003F	see Table 5	2.4	1.1	-0.9	4.5	1.2	2.5	3.2	-0.6	-1.3	-1.5	-1.2	-1.1	
37	15	AA869173_defensin-related_cryptin	see Table 5	-1.2	1.1	-1.2	1.6	1.6	2.2	1.3	1.6	1.1	1.6	1.6	1.6	
39	16	AA631172_defensin-related_cryptin	see Table 5	-2.9	1.1	-1.2	1.1	1.6	1.2	-2.2	1.2	-1.1	-1.2	-1.2	-1.1	
311	17	AI893944_defensin-related_cryptin	see Table 5	-1.7	-1.0	1.7	1.9	1.3	1.2	1.1	1.3	-1.1	-1.1	-1.1	-1.1	
236	14	AA619953_ESTs_Weakly similar to P25027_hypothetical_protein_T20D3.2	see Table 5	-1.6	1.3	1.4	1.3	1.6	1.2	-1.5	-1.4	-1.3	-1.3	-1.3	-1.6	
8	19	AA034578_chordin	see Table 5	-2.3	1.0	1.2	1.6	1.2	1.4	1.3	1.2	1.1	1.1	1.1	1.1	
49	20	AA77591_Mus_musculus_11_IDs_3	see Table 5	1.1	1.0	1.4	1.1	1.5	1.5	1.6	1.2	1.1	1.1	1.1	1.1	
71	21	AA827958_scorpionin A-1	see Table 5	-1.9	-1.3	-1.1	-1.4	-1.4	-1.7	-1.3	-1.6	-1.2	-1.1	-1.1	-1.1	
48	1	AA619407_nucleoside-associated protein	see Table 5	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	

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312	2	AA237986_cytchrome_P450_3a25	Homo sapiens cytochrome P450 variant 3A7 (CYP3A7) mRNA, complete cds; gi-12082808//Human_Jongleur_201102.8196.ting	0.9	0.2	0.4	-0.1	0.0	-0.4	0.2	0.2	0.1	0.0	0.3
31	3	W56983_periplasm_mycelin_protect_22_kDa	see Table 5	0.5	0.0000	0.4	0.1	0.0	0.0000	0.1	0.0	0.2	0.1	0.2
290	4	AA107035_guanylate_cyclase_activat or 2b (recom)	see Table 5	-0.2	-0.3	0.1	-0.1	0.0	-0.5	-0.0	-0.2	-0.2	-0.5	-0.2
53	5	AA110836_nucleotidiers	see Table 5	-0.1	0.0000	-0.1	0.3	0.0	-0.3977	0.0	0.0	0.1	-0.1	0.0
314	6	AA109873_RIKEN_cDNA_0510010 BB5 gene	Homo sapiens bryothelial protein FLJ10830 (FLJ10830), mRNA; or gi-9322698//Human_Jongleur_201102.8671.C2	-0.1	-0.1	0.1	-0.9	0.0	0.0	0.0	0.0	0.0	-0.1	0.0
315	7	AI323162_dipeptidase_1 (recom)	Homo sapiens dipeptidase 1 (recom) (DPEP1), mRNA; or gi-4758189//Human_Jongleur_201102.8623.C1	0.2	-0.3	-0.4	0.0	0.0	-0.4	-0.3	-0.1	0.0	0.0	-0.3
41	8	AA871838_phospholipase_A2_group 1b (platelets, synovial fluid)	see Table 5	-0.1	-0.0	-0.2	0.0	0.0	-0.0	-0.0	0.0	0.2	0.3	0.0
24	9	AA666394_RIKEN_cDNA_11100233 15 gene	see Table 5	0.0	0.3	0.1	-0.4	0.0	-0.4	0.1	-0.0	0.3	-0.2	-0.2
304	10	AA556694_cytchrome_P450_2b9_c phenanthrolic indazole, type a	see above	-0.1	-0.4	0.2	0.3	0.0	-0.3	0.1	-0.3	0.2	0.1	-0.2
46	11	WI5890_guanylate_cyclase_activat or 2 (guanylin 2_intestinal, leuconide)	see Table 5	0.0	0.0	-0.3	0.2	0.0	-0.5	-0.1	-0.3	-0.0	-0.1	0.4

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[illegible]

Table 6 Page 10



Table 6 Page 12

[illegible]

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64	6	AA81013_oryzotoma_P450_2637	see Table 5	1.9	4.1	3.8	3.1	3.2	3.6	3.9	3.1	3.1	3.2	3.8
		Human mRNA for liver alcohol dehydrogenase (EC 1.1.1.1) gamma 2 subunit from AD1D locus at: g1-284530/												
329	7	AL507919_alcohol_dehydrogenase_1_complex	[Human_Jongleur_20102.12404.s1.g162]	1.6	4.2	3.9	3.4	3.5	3.4	3.8	3.1	3.1	3.2	3.3
				1.6	4.2	3.9	3.4	3.5	3.4	3.8	3.1	3.1	3.2	3.3
65	8	AA52452_alanine_carrier_family_27_(fatty_acid_transporter)_member_5	see Table 5	1.7	4.3	3.7	3.5	3.8	3.7	3.7	3.1	3.1	3.3	3.2
		orth. Homo sapiens synaptosomal complex member 5 (SYCP5), mRNA												
		cc:1524235790/	[Human_Jongleur_20102.4239.C3]											
			: h. Jongleur(strom)											
330	9	AA74336_synaptosomal_complex_p16.1_AA74336	AA74336_synaptosomal_complex_p16.1_AA74336	3.8	3.2	3.8	3.4	3.5	3.5	3.1	3.4	3.2	3.3	3.3
		Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 2 (SLC2A2), mRNA or g1-45575500/												
331	10	AA27317_alanine_carrier_family_2_(facilitated_glucose_transporter)_member_2	[Human_Jongleur_20102.11033.C1]	3.9	3.1	3.9	3.1	3.4	3.8	3.6	3.2	3.2	3.3	3.3
				3.9	3.1	3.9	3.1	3.4	3.8	3.6	3.2	3.2	3.3	3.3
319	11	AA63765_metallothionein_1	see above	1.9	3.1	3.2	3.2	3.2	3.2	3.2	3.2	3.2	3.2	3.2
56	12	AA10217_gre-B-cell_colony-enhancing_factor	see Table 5	3.2	4.2	3.7	3.9	3.6	3.6	3.4	3.9	3.9	3.9	3.9
245	13	AA274023_apoptosis_inhibitory_6	see Table 5	3.3000+	4.0020+	3.7	3.9	3.800+	3.800+	3.800+	3.800+	3.800+	3.800+	3.800+

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## Claims

1. A method of diagnosing a cancer in a subject comprising determining, in a sample from the subject, the level of at least one polypeptide, wherein a higher level of the polypeptide compared to the level of the polypeptide in a subject free of cancer is indicative of cancer, and wherein the polypeptide is selected from the group consisting of:
  - a) polypeptides encoded by the polynucleotides listed in Table 5; and
  - b) polypeptides which are at least 70% homologous to the polypeptides of a).
2. The method of claim 1 wherein the sample is taken from a bodily fluid.
3. The method of claim 2 wherein the bodily fluid is selected from the group of fluid consisting of blood, lymph fluid, ascites, serous fluid, pleural effusion, sputum, cerebrospinal fluid, lacrimal fluid, synovial fluid, saliva, stool, sperm and urine.
4. The method of claim 1 wherein the level of the polypeptide is determined by a method selected from the group consisting of immunohistochemistry, western blotting, ELISA, antibody microarray hybridization and targeted molecular imaging.
5. A method of diagnosing a cancer in a subject comprising determining, in a sample from the subject, the level of at least one polypeptide, wherein a higher level of the polypeptide compared to the level of the polypeptide in a subject free of cancer is indicative of cancer, and wherein the polypeptide is selected from the group consisting of:
  - a) polypeptides encoded by the polynucleotides listed in Table 6; and
  - b) polypeptides which are at least 70% homologous to the polypeptides of a).
6. The method of claim 5 wherein the sample is a tissue sample.
7. The method of claim 6 wherein the tissue is selected from the group of tissue consisting of brain, lung, liver, spleen, kidney, pancreas, intestine, colon, mammary gland or breast, stomach, prostate, bladder, placenta and uterus.
8. The method of claim 5 wherein the level of the polypeptide is determined by a method selected from the group consisting of immunohistochemistry, western blotting, ELISA and targeted molecular imaging.

9. A method of diagnosing a cancer in a subject comprising determining, in a sample from the subject, the level of at least one polypeptide-encoding polynucleotide, wherein a higher level of the polynucleotide compared to the level of the polynucleotide in a subject free of cancer is indicative of cancer, and wherein the polynucleotide is selected from the group consisting of:
  - a) the polynucleotides listed in Table 6;
  - b) polynucleotides having sequences that differ from the polynucleotides in (a), without changing the polypeptide encoded thereby; and
  - c) polynucleotides which are at least 70% homologous to the polynucleotides of (a).
10. The method of claim 9 wherein the sample is a tissue sample.
11. The method of claim 10 wherein the tissue is selected from the group of tissue consisting of brain, lung, liver, spleen, kidney, pancreas, intestine, colon, mammary gland or breast, stomach, prostate, bladder, placenta and uterus.
12. The method of claim 9 wherein the sample is a is taken from a bodily fluid.
13. The method of claim 12 wherein the bodily fluid is selected from the group of fluid consisting of blood, lymph fluid, ascites, serous fluid, pleural effusion, sputum, cerebrospinal fluid, lacrimal fluid, synovial fluid, saliva, stool, sperm and urine.
14. The method of claim 9 wherein the level of the polynucleotide is determined by a method selected from: RT-PCR analysis, in-situ hybridization, polynucleotide microarray and Northern blotting.
15. A method of measuring the responsiveness of a subject to a cancer treatment comprising determining the level of at least one polypeptide in a sample taken from the subject before treatment, and comparing it with the level of said polypeptide in a sample taken from the subject after treatment, a decrease in said level indicating responsiveness of said subject to the cancer treatment, wherein the polypeptide is selected from the group consisting of:
  - a) polypeptides encoded by the polynucleotides listed in Table 5 and Table 6; and
  - b) polypeptides which are at least 70% homologous to the polypeptides of a).
16. The method of claim 15 wherein the sample is taken from a bodily fluid.
17. The method of claim 16 wherein the bodily fluid is selected from the group of fluid consisting of blood, lymph fluid, ascites, serous fluid, pleural effusion, sputum, cerebrospinal fluid, lacrimal fluid, synovial fluid, saliva, stool, sperm and urine.

18. The method of claim 15 wherein the level of the polypeptide is determined by a method selected from the group consisting of Western blotting, ELISA and targeted molecular imaging.
19. A method of measuring the responsiveness of a subject to a cancer treatment comprising determining the level of at least one polypeptide-encoding polynucleotide in a sample taken from the subject before treatment, and comparing it with the level of said polynucleotide in a sample taken from the subject after treatment, a decrease in said level indicating responsiveness of said subject to the cancer treatment, wherein the polynucleotide is selected from the group consisting of:
  - a) the polynucleotides listed in Table 6;
  - b) polynucleotides having sequences that differ from the polynucleotides in a), without changing the polypeptide encoded thereby; and
  - c) polynucleotides which are at least 70% homologous to the polynucleotides of a).
20. The method of claim 19 wherein said sample is blood or bone marrow cells.
21. The method of claim 19 wherein the level of the polynucleotide is determined by RT-PCR analysis.
22. The method of claim 15 or 19 wherein the treatment is administration of a chemotherapeutic drug.
23. The method of claim 15 or 19 wherein the treatment is radiotherapy.
24. The method of any one of claims 1, 5 or 9 wherein a change in the level of the polynucleotide or polypeptide as compared with the normal level is indicative of an abnormality in a tumor suppressor gene or a biological pathway in which a tumor suppressor gene is involved.
25. The method of claim 24 wherein the tumor suppressor gene is selected from the tumor suppressor group consisting of p53, Rb1 and PTEN.
26. The method of any one of claims 1, 5 or 9 wherein a change in the level of the polynucleotide or polypeptide as compared with the normal level is indicative of the effectiveness of a drug that modulates the activity of a tumor suppressor gene.
27. The method of claim 26 wherein the tumor suppressor gene is selected from the tumor suppressor group consisting of p53, Rb1 and PTEN.
28. A method of identifying a diagnostic marker for a cancer comprising:

- a) obtaining a first cell from a first cell type of said cancer, said cell comprising a defective tumor suppressor expression;
  - b) obtaining a second cell of the first cell type, wherein said second cell comprises a wild-type tumor suppressor expression;
  - c) identifying genes having an increased level of expression in the first cell as compared to the second cell; and
  - d) selecting at least one gene of step c) as a diagnostic marker for the cancer.
29. The method of claim 28 further comprising:
- a) obtaining a first cell from a second cell type of said cancer, said cell comprising a defective tumor suppressor expression;
  - b) obtaining a second cell of the second cell type, wherein said second cell comprises a wild-type tumor suppressor expression;
  - c) identifying genes having an increased level of expression in the first cell of the second cell type as compared to the second cell of the second cell type;
  - d) comparing the genes having an increased expression in the first cell type with the genes having an increased expression in the second cell type;
  - e) identifying genes having an increased expression in the first cell type but not in the second cell type; and
  - f) selecting at least one gene of step (e) as a diagnostic marker of a cancer of the first cell type.
30. The method of claim 28 or 29 wherein the tumor suppressor gene is selected from the tumor suppressor group consisting of p53, Rb1 and PTEN.
31. The method of claim 28 wherein the identification of step c) is performed using a microarray.
32. The method of claim 29 wherein the identification of step e) is performed using a microarray.
33. The method of claim 29 wherein the identification of step c) and e) are both performed using a microarray.
34. A method for screening for compounds that modulate the activity of a tumor suppressor gene comprising:
- a) obtaining a cell comprising a defective tumor suppressor expression;
  - b) measuring the level of expression of a marker of Table 5 or 6 in the cell;
  - c) contacting the cell with a test compound; and
  - d) measuring the expression of the marker of step b) after the contacting step c), wherein a change in the level of expression after said contacting step as compared to the level of expression before said contacting step is indicative of the ability of the compound to modulate the activity of the tumor suppressor gene.

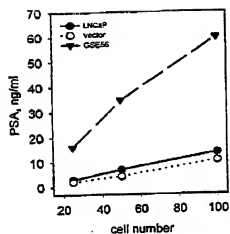
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35. The method of claim 34 wherein the change in the level of expression in step c) is a reduction in the level of expression.
36. Use of compounds identified according to the method of claim 35 in the treatment of cancer or as anti-cancer drugs.

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**FIGURE 1**



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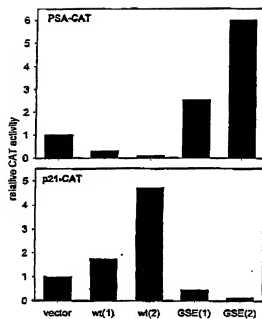
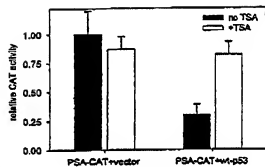


FIGURE 2

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**FIGURE 3**

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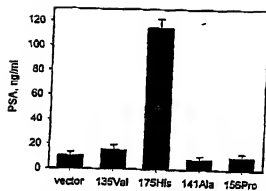


FIGURE 4

Figure 5

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>gi|10190652|ref|NM|003901.1| Homo sapiens sphingosine-1-phosphate lyase 1 (SGPL1), mRNA [SEQ ID NO:
1]
5  CCTGCGAGTCGTCGCGTGCCTGAGGGAGACGACGAGGTGGAGCCGCCCGGGTGTCTCGAG
GGGAAGGACGCGAGGGGTGGAGCCCGCGCGTCTCTGAGGAGGAGACTGGAGAGCTGGTT
CCGGCTCTGAGGAGAGTCTGAAAAGGGGAGCGAGGAGGCTGAGGAGGAAGTGA
CCTGAGCAGAGACCTTCTGATGTTGAAAGCCCTTTGCGCCTACTTATGAGATTTTGGAAGTA
10  TATCTCCAGAAAGGACCAAGATTTATGTAATGGACATTCACCAAGATATAGAGCCCTGGAGCA
CTAATTCGATGAGATCTGAGAAATGTGTGAGACTCTGATGCGGGATGATGATTTCTGCTG
CAGCCAGCAGAGTTATGTGCTCAAGGTATAAAGCAAAATGTTTAAAGCTCACCCAGGAAGTG
CCCATTATTGTGCTGAAGATTCAAGACAAGTTGAAACAAGCCAGGATGATATTAGCAAG
AACATGTCAATCTCGTAAAGTGGACAAGAGTATGTGAAGCTTTAACCTCCAGGGTCTG
AGCTCATCTGCTGTTTGGAGAACTTAAGGACGACGCTCATATGAGCGCCTCTGCGCAA
15  GAGGGGAGAGCCTCTGGAACAAGTGTACAGTGGGGAGGAGAGCTCACTGAAGCTCTGTG
AAGGTATGAGGATTTTGAAGAGTAAAGCCCTGATCCAGATATCTCCAGGACTA
CCGAAATGAGGAGAAATGTGAGGTAGCTTTTCTCTTTCAATGGGGAGCAAGAT
TCGTGTGATGTGTGACTCTCTGGGGAGACAGAAAGCATATCTGATGCGCTCAAGAGCATAT
CGGATCTGGCTTTGAGAGGGGATCAAACTACAGAAATTTGTGCTCCCAAGTGC
20  CATGCTGCATTTAAACAAAGCAGCGATTTACTTTGGATGAAGATTGTGGGGTCCCATGTG
ACGAAGATGATGGAGTGGATGTGCGGCGAATGAGAGAGCTATCTCCAGGAACCTGCC
ATGCTGCTGCTGTTCTACCCCAAGATTTCTCATGGTGTAAATAGATCCTGTCCCTGAAGTG
GCCAAGCTGAGCTCAAAATCAAAATACCTCTCATGTGACAGCTGTTGTCTGGAGGCTTC
25  CTGCTCCTTTATGAGAAACAGAGATACCCCTAGGAGACCATTTGATTTCCCGGT
AAAGGTGTAACAAGCATTTCAAGCTGACACCCATAATGATGGCTATGCCCAAAAGGCTCA
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30  CGAGCTGCTGGCTGCTGTTGATGACTCTGGTGAAGACGGCTATGTTGAAGCTACCAAA
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AATGGTCTCCAAACCCCACTGAACTGTGAGCCCTTTCTAGTCTCAAGGGGATTCAGCC
TTCHAGAGATTTCTGGATATGGAACAGGCGGTGACACACTTTGACATCTGTGCTGTGCTG
40  CATGAGCAGTCTAGATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATG
CTCTATCTCTCTTTGTGGTTTAAATTTGAAGACCCAGAGAAATCCATACATATAG
ATTTTGCCTTTGTATAAATGTTTACCTAGG
>H_1.0.0_131819 Homo sapiens mRNA for putative cytoplasmatic protein (ORF1-FL21) as: gi-12214172///
[gi|12214172|emb|AJ245876.1|HSA245876] [SEQ ID NO: 2]
TATGACAGGCGATGACTGAGTTCAATGTAAAGTTACCAAGTCAATCTGCTCTCCCTCTCT
CCCAAGAGTCAAAATTTCCGAAATGCTGAGTCTGCTGCTGCGAGGAGTGAAGGGTTGC
45  TACCTATCTTTTATGATCTCTCTCAAGCCTCTCTCAATGCTCATCAATGATATGATGAGT
TAAACCAAGGAGCTATTTCTGACACAGCAATTTTGAAGCGGCAATTTGCCAAATACCAAC
AAGTTCACTCTCCAGTAGGAAGATAGAGAACCTCTTGCAAAATTTCAAGCATC
TACAGAGGAGATTTTCCAGAAATTAAGACACTGGCTGAGCTCTCAAGAGATGTTTCAGG
ATGTCATGTTCTACAGTATCTGGCCTATGCTCAGACAGAGGGGCTCTACAGGACCTGA
50  TGAATCATGCTGGAATTTGACAGCTCAGGTCATTTGGATGGCCCTGGTGTGTCATCCTAA
AGAACTCAAGAGGATTAACCACTGATGTTTAAACCAAGAGACCCATCTTTATC
GTTCTGAAACCATGAGTCTGAGTGTGATCTTCAACAGCATTTTCTGGCTTTCAATG
AGAAAGAGATCTCTCTCAGCAGAGGATGATAGAGCATCTGTTGAGCCAACTTCA
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55  AGGGTTTGGCCATCACTATGGCGCTCTGCAAGAGTGTGGCTTAGAGYAGAGCTGGATA
ACCCAGGTCAACCTGGGATGAGAGCAAGATGCCCTCTGCTGCTCTATGGGATC
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TGTGCTCTCTGCTCTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG
60  GTTTCTGGGTGTGGAATATCTCTATATTTGACAGAGTTTATATATGAGNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
>H_1.0.0_21316 Homo sapiens claudin 8 (CLDN8), mRNA cr: gi-21314655///
[Human_fongleure_201102.9749.CL] [SEQ ID NO: 3]
65  GTTCATTATCAAGGAAACATGTTCTCTCTCTGTGACAGAGAAACCTGCTCAAGACA
GAGTATGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG
TGCTTTGAAGATCCGTGGCTGTTCTGCTGGTGTGGAATGTGGGACAGCTGCTGCTGT
CACTGTATGCTCTGAGTGGAGATGTGCGGCTTCATTGAAACACATCTGTTTGA
AACTTCTGGAGAGATCTGGATGAATGCGTGAAGCAGCTCAATCACTAGGATGCAGTG
70  CAAATCTATGATTCCTGCTGCTCTCTCTGCGGCTACAGGACCGAGGACTGAT

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 CAAAATTGATGAACTGACATCCAAATTTGAAAGTTTGTGTGACGCTGTCTAGCTTAA  
 ATGAATTTGTTCTATTGCTTTATACATTTATATTAATAAATGTGACATTTTCTAATTA  
 TTTG

M\_1.0\_17482 Mus musculus L89 gene, partial sequence cr: gi-687696///  
 [Mouse\_jongleur\_201102.10974.Cl] [SRQ ID No: 4]  
 GAATCTAGAAAGAACTTACATGAGCTGCTGGTATACTATAAAGCAATTTGGTGGCAAA  
 GATAGGAGCATGGTTTGAACATGGCTGCGAGGACAGAGGTGAAGCAGAGCGGTACCC  
 AGTCTACAGACTGAACAGAGCATTTGCGAGGACAGAGGAAAGGCTTTTCACTGTGGT  
 GGTATGCCATGCTTTCTCGAATAAAGAAATACAGCCAGAGAAAGGATTAAGTGGACATAG  
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 CACGAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG  
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[illegible]

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ACAGTACTATCTGATACAACTCCAGAGGAGAGACCCCTGTGTGCTG  
25 H\_1.0.0.11184 Homo sapiens intelectin (ITLN), mRNA cr: gi-8923027///  
[Human\_jongleur\_201102.4257.C2] [SEQ ID NO: 42]  
AGGAGCGCTTTTGGAGAAAGCTGCACTCTGTGTAGCTCCAGGGCGCAGTGAAGGAGGGA  
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30 CTAACTACTCTTGGAGAGAGACCTGTTCTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT  
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TGGCCAGGTGCTATGAGATGACATGGTGGGAAGTGCAAGGTGGCGATGCTGTGTCCTCA  
35 GTGCAAGGGCAGCAAAAGCAGACTACCCAGAGGGGAGACCGCACTGGGCCAATACACACA  
CCTTTGGATCTGCAAGAGCGCCACAGAGGATGACTACAAAGAACTGGCTACTGACAGACA  
TCCAGAGCCAAAGAACCTGGGCATCTGGCAAGCTGCCCAATATGCCCTCATGACAGCTGGA  
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40 ATCTGTTTGGCTCTACAGAAATATCCAGTGAATATGAGAGAGAAATGTGTGAGACTG  
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45 AGCACTGAGCACTGATGAGAGGATACTTTCCAGAGCGCACTCCGACAGTGTGGAG  
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H\_1.0.0.7658 Mus musculus defensin related cryptdin 5 (Defcr5), mRNA cr: gi-6681172///  
[Mouse\_jongleur\_201102.3937.C3] [SEQ ID NO: 43]  
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TGCAGAAATCTTTTAACTTTGTATTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT  
60 H\_1.0.0.23593 Highly similar to NEP\_HUMAN Neprilysin (Neutral endopeptidase) (NEP) (Enkephalinase)  
(Common acute lymphocytic leukemia antigen) (CALLA) (Neutral endopeptidase 24.11) (CD10) [H.sap cr:  
gi-8169687] [EST390530 Homo sapiens cDNA /gb=AF978421 /gi=8169687 /ug=Hs.307734 /len=675.  
[Human\_jongleur\_201102.11097.C4] [SEQ ID NO: 44]  
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55 CTCACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT  
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60 CTGCGAGATTTCTGCAAAAGTCCAATACTGAAATGCTTGGCTGAGCTGTGCACATCTGTTT  
TAATGGAATTAACCGCACTACTGTGGCTATAGTTTCCACACCACTGTGCGAAGTTCGA  
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70 TTTTAAATATCTTGTATAGCTCTGTATGCTGTGACAGAGCTCTCAATATGCAAGT  
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GGGTGATTTCTGTCTCTATGACATGCGGATGCCCATAGTTCAATGAGTGTGAGCTGCT  
GGGCACTTAAGAGAGGGGGGCTGAGATGCCCGCTGGGAGACTATGATTTCTCTCTGCT  
75 AAGATTAATGCTAGTACAGCTGCTCACTATCACTCACTCTTTCTCACTTTT  
CTCGGAGCTTCTCAGTGTGTTTACTTNGCTGAATTTCAAAATTTGAATATGTTCTCTCGA

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>H.1.0.0.22550 Homo sapiens Bsnhl domain (SCR repeat) containing (BK65A6.2), mRNA cr: gi-22095356///  
[Human\_jongleur\_201102.10520.Cl] [SEQ ID NO: 52]

5

GCCTGGAGGCACTGCATGCTGGCTGCAGACACAGGCTGCACCATGAAGCCAGCCCTCC  
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10

CGACGCTGCTCTGGCCTTGCGCACTGCTCTGGATTTCCGGGACTTCTGCTCGGAGATAT  
TGCCCTACTCAGGATCCATGATGGGGCGAAGGACTTGTGGTGGGCACTTCAAGATGT  
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15

ATGTGGACTCTCTGAGATCTGACAGCAAAATATACGAGGCGAGAGAGCTGTGAGGCGC  
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CTGTGACCCACCAAGTGTCAATGATGGAGAGAGGAGCTTGTGTGAAGAGAGACGGCTT

20

GGCAATCTAGCGGACCGCGTAACTCTCAGGCAAACTCAGGCTGACCTGGATCTCAAGT  
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25

ACTCCGGCTCTTCACTTTACCCCAAAACTTGTCTCTCCAGACTACAGAGATATGGGCG  
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30

TGGCTTGGGCAAGAACTCAGTGGCAGGCTGGGAGGAGCTGGAGGATCAGCTGCCCAACT  
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35

GGGCGCTGCATGTGTGCTTCTGTGCAAGCGAGCTCGGTAAGGCTCAGGTCAAGTCAAGT  
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40

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45

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50

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55

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TCCTGGTCAAGACTCTGTATACAACTCAGGCTCAAGGAGGCTCTTGAAGCTGTGAGCTG  
CCAGATGAGCCACCTCTCAACCCAGCGAGGAGGCGCAAGTGTCTCAACACCCAGCCGCTG

60

CTACCTTACTTCCACTGTGACAAAGGCTACAGCTGGCGGGGCGAGGACAGCACTGTGCC  
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65

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AGCTTGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGT

70

CGGCTTCCGCACTTCAAGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGG  
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CTAGGCTTCCAGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGG

[Human\_jongleur\_201102.3017.Cl]

>H.1.0.0.8885 Homo sapiens amnionless protein (AMN), mRNA cr: gi-13569914///

[SEQ ID NO: 53]

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TTCCCGAGCGAGAGATGTGTCTGCTCTGGTGGCAAGAGGTCAAGCGCTCTCAGACATG  
TCTCTGCGCTGTGATGGGAGACTGTCTGTGCTCAGGAGCCGAGATTTGGGCTCTCAGAC  
GTGGGCTCGACACTTGGACTGTGGGCGGGGAGGCTGTGGGCTGTGGGCTGTGGGCTGTGGG

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CTGGACTGCAGCGTCTGTACTTCTGTACACGACCCCACTACATCGATGACATCA  
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 >H\_1.0.0\_14511 Homo sapiens pre-B-cell colony-enhancing factor (PBEF), mRNA cr: gi-5031976//  
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 [Human\_jongleur\_201102.6032.C2] [SEQ ID NO: 57]  
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 >H\_1.0.0.17326 Homo sapiens mRNA for MCM10 homolog, complete cds cr: gi-11527601///  
 [Human\_jongleur\_201102.7564.C2] [SEQ ID NO: 62]  
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TAAGAGTGGCACTTTAAGAAAGTGACTACTTCATGCCTTTCTCAGCAGGAAAAACGGAT  
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>H.1.0.0.23524 Homo sapiens cytochrome P450, subfamily IIC (mephemtoin 4-hydroxylase), polypeptide 19 (CYP2C19), mRNA cr: g1-4503218/// [Human\_jongleur\_201102.11077.C2] [SEQ ID NO: 64]

CTCCAAATGACCTTTTGTGCTCTGCTCTGCTCTGCTCAATGTTCTCTCTCTCTCTCA  
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>H.1.0.0.11755 Homo sapiens solute carrier family 27 (fatty acid transporter), member 5 (SLC27A5), mRNA cr: g1-13325056/// [Human\_jongleur\_201102.4565.C1] [SEQ ID NO: 65]

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TCTGGCCCCAAGTTCCTACTCTCTGCTCTGCGATGACTGTGGCAGCATGGCGTGAC  
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5 CAACATGGGCTTAGTCAACTATGTGGGGCGCTCGGGGCGCTGGGCANAGTAGCTGACCT  
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15 CACCAAGCATTTCAACTGATGAGAGAGCCGGTGTGTGTGAGGGCTTCAATGTGGAGAT  
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25 TAAAT  
>gi|3743331|gb|AI191212.1|AI191212 qc95h03.x1 Soares\_pregnant\_uterus\_Nb1PU Homo sapiens cDNA clone  
IMAGE11722005 3', mRNA sequence [SRQ ID NO: 67]  
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35 AGGTAAAGAGAGAGTCTGTGGT  
>H.1.0.0.5007 Homo sapiens selenoprotein P, plasma, 1 (SRP1), mRNA cr: gi-4885590//  
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60 ATTGTGCAACATGAGAAATCTACTGATTTGGCTTCCAGATTAAATTTTAAATTTTATGTCAT  
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70 AAGATATAGGGAAGAAATATATGTGTCTCTTATATGCTTGTAGTAAATTTTCAAT  
GTCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT  
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 10 GTATPACGCAAGATGCGCAGCAGCAAGCTGTCTCCCGATCTGATCTCTGGATCT  
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 20 AATGTCCAGGCCGTGATCAGCGACATCTGCTCTCCCTGGAGAGACGCTTCCCTCTACTTCA  
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 thiolase) (ACAA2P), nuclear gene encoding mitochondrial protein, mRNA cr: gi-5174428///  
 35 [Human\_jongleur\_201102.11645.C1] [SEQ ID NO: 70]  
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 70 [Human\_jongleur\_201102.263.C2] [SEQ ID NO: 71]  
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>H\_1.0.0.21557 Moderately similar to HEMI\_HUMAN 5-aminolevulinic acid synthase, nonspecific, mitochondrial precursor (delta-aminolevulinic synthase) [O cr. gi-5850819///ws61h08.xl Homo sapiens cDNA 3' end /clone=IMAGE.2501727 /clone\_end=3' /gb=AW003903 /gi=5850819 /ug=hs.407036 /len=678. (Human\_jongleu.201102.9885.C2) [SEQ ID NO: 75]

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>H\_1.0.0.5587 Homo sapiens carboxylesterase 3 (brain) (CES3), mRNA cr: gi-6912297/// (Human\_jongleu.201102.1674.C1) [890 ID NO: 76]

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 >M.1.0.0.20499 Mus musculus 13 days embryo forelimb cDNA, RIKEN full-length enriched library,  
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 sH\_1.0.0\_23668 Homo sapiens BCL2/adenovirus E1B 19kDa interacting protein 1 (BNIP1), transcript  
 variant BNIP1, mRNA cr: gi-4502440/// [Human\_jongleur\_201102.11130.C4] [SEQ ID NO: 114]  
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 >H\_1.0.0.125911 Homo sapiens nucleophosmin (nucleolar phosphoprotein B23, numatrin) (NPM1), mRNA cr:  
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 40 G  
 >H\_1.0.0.37314 Homo sapiens cDNA FLJ38286 fis, clone FCBF3008153, highly similar to ALPHA-AMYLASE  
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gg|182057|g|H16492.1|HUMELAP2 Human pancreatic elastase IIA mRNA, complete cds [SEQ ID NO: 119]  
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>H\_1.0.0.10916 Homo sapiens hypothetical protein FLJ10563 (FLJ10563), mRNA cr: gi-8922518//  
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>H\_1.0.0.72558 qc9608.x1 Homo sapiens cDNA 3' end as: gi-3743449// [clone=IMAGE:1721110  
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>H\_1.0.0.17762 Homo sapiens KIAA1576 protein (KIAA1576), mRNA cr: gi-24308256//  
[Human\_jongleu\_r\_201102.7803.C1] [SBQ ID NO: 122]

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>gi|15689855|gb|BI714160.1|BI714160 ie33g03.x1 Kaestner ngn3 wt Mus musculus cDNA 3', mRNA sequence  
[SRQ ID NO: 160]  
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ACTGTGGGCAATATAGTCTGAGCATGTCTTAAACAGTGTCTGTGATATCTAGAG

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TCAGATATACATATGTCAGGAAGGGAAGTGAACATTCCTCTAAGAAAGCACTCCCGTT  
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ATATAAGCTTAGGAATTTATGCGACCAAGCACTTGCTCTCCTCCTCATTGGCTCGGGGGCTT  
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AAACTGTCA

>H\_1.0.0.2912 Homo sapiens interleukin 13 (IL13), mRNA cr: gi-4504644//  
[Human\_jongleur\_201102.525.C1] [SEQ ID NO: 161]

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TGTACTGTGACGCGCTGGAAATCCCTGATCAACGTGTCAAGCTGTGAGTCCAGTCCAGTGGAGA  
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>H\_1.0.0.7164 Mus musculus killer cell lectin-like receptor subfamily A, member 21 (KLR21), mRNA  
cr: gi-21361215// [Mouse\_jongleur\_201102.3652.C9] [SEQ ID NO: 162]

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>H\_1.0.0.14332 Homo sapiens step II splicing factor SLU7 (SLU7), mRNA cr: gi-20127500//  
[Human\_jongleur\_201102.5919.C1] [SEQ ID NO: 163]

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[illegible]



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 >H\_1.0.0.27645 Homo sapiens Ku70-binding protein (KUB3) mRNA, partial cds cr: gi-4878033///  
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>H.1.0.0.12524 Homo sapiens hypothetical protein BC013764 (LOC115207), mRNA cr: gi-19923972//  
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10 >H\_1.0.0.579 Homo sapiens hypothetical protein MGC26914 (MGC26914), mRNA cr: gi-21699059///  
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45 >H\_1.0.0.22812 Homo sapiens hypothetical protein MGC18216 (MGC18216), mRNA cr: gi-22748948///  
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TTTATACACACTATTGTAGCTTCTTAGGTTCATAGGTAGCGTTTCAAGTAGTTGACI  
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>H\_1.0.0.21542 Human mRNA for cardiac troponin I or gi-37427/// [Human\_jongleu\_201102.9882.C3]  
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60 TGAGCTGA  
>H\_1.0.0.125034 Moderately similar to CLUS HUMAN Clusterin precursor (Complement-associated protein  
SP-40,40) (Complement cytolysis inhibitor) (CLI) (NA1 and NA2) (Apolipoprotein J) (Apo-J) (TRPM-2)  
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GAGACCGGAAGGTTAAGTACTGTCTCGNCCCTGTGTGAAGGTTAGGCCACTGGGAACCC  
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15 >H\_1.0.0\_2410 Homo sapiens death-associated protein kinase 3 (DAPK3), mRNA cr: gi-4557510///  
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55 CCAGAT

>H\_1.0.0\_60977 Homo sapiens, KIAA0186 gene product, clone MGC:13345 IMAGE:4333095, mRNA, complete  
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 >H\_1.0.0.15972 Homo sapiens proteasome (prosome, macropain) inhibitor subunit 1 (P131) (PSNFI), mRNA  
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>H.1.0.0.40132 Homo sapiens golgin-245 mRNA, complete cds nt:  
[Human\_jongleur\_201102.cl.746\_single] [SEQ ID NO: 238]  
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>H\_1.0.0\_2653 Homo sapiens lipase, hepatic (LIPC), mRNA cr: gi-4557722///  
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>H 1.0.0 19679 Homo sapiens CD5 antigen-like (scavenger receptor cysteine rich family) (CD5L), mRNA
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65 SH 1.0.0 24569 Homo sapiens transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin C) (TCBB1), mRNA cr: gi-16933562/// [Human tongue 201102.11637.C2] [SEQ ID NO: 250]



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>H\_1.0.0.9423 Homo sapiens cDNA FLJ10331 fis, clone NT2RM2000635, highly similar to Homo sapiens  
mRNA for KIAA0729 protein cr: gi-7022294/// [Human\_jongleur\_201102.3321.C2] [SEQ ID NO: 276]

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>H\_1.0.0\_12336 Homo sapiens deoxyguanosine kinase (DGUOK), transcript variant 1, nuclear gene  
encoding mitochondrial protein, mRNA cr: gi-18426966// [Hman\_gongleur\_201102.4322.C2] [SRQ ID NO:  
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 70 ATTTCTGCTGACTCTACTATTAAGTTTGAATAATGTTTACCTTCAAGCAAGATATTTCT  
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TTCTGGCATAACTAAATTAAGTATATATATTGGCTCAATAAATTTG  
 >gi|2462368|gb|H160918.1|H160918 UT-M DJ1-bcy-2-10-0-UI.s1 NIH\_BMAP\_DJ1 Mus musculus cDNA clone  
 UT-M-DJ1-bcy-2-10-0-UI 3', mRNA sequence [SBQ ID NO: 289]  
 5 TTTTITTTTTTTTTTAACTGTGCGATGTAGGTAGATTATTTTAAAGCGAAGAGGG  
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 GAGGAGGGTCAGAAAGGCTGATGGGAGGTAAAGTTGGCTCTCTGGGTGGGGAGGATG  
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 10 CTGATTTGCAAAAGAGAGGATCTGCTGACAGACAGTCTCAAGTGGCTCTCA  
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 >H\_1.0.0.4965 Homo sapiens guanylate cyclase activator 28 (uroguanylin) (GUCA28), mRNA cr: gi-  
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 15 GACGACGCGAGGAGAACCCAGGAGGAGCGGATGGGCTGAGAGGCTGCGTCAAGGCTCTCTG  
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 20 CTCTGCTCAGGACCTTCAGCCTGTCTGCGCTCGCAGGAGGCTTCAGCATCTTCAAGA  
 CCTCTGAGGACCATGCTAAAGCAAGCATGTGAGCTGTGTGAAAGTTGGTGTACCGGCT  
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 25 GGAGGGGAGGCGCTCGAGGCGCCGCTGATCTGATATAAGATTTCAACACAGG  
 >M\_1.0.0.7865 Mus musculus uterine-specific proline-rich acidic protein (Upa), mRNA cr: gi-6678510///  
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 45 GAGAGCTGTATGCAAGTGGATTTTCTTCACTGACCTCTGAGGACAGAGTCTGACATG  
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 50 TTTGAAATGGGAAGCCAGACTCTATCTCATCAAAAATCTGGGCGCTTGTGAGAA  
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 AAGACAGCAGAGGCTTCTGATGACATCACTATGAGATGGCAGGACTGATCCCTG  
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 65 CTTATCATCCAGTGAATGAGACCGGAAGCAGCTGATGGAGAGACTCAGGCGCATGACT  
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AACCGGACCTCAGGCTTAGGCAAAACCCCACTGTGGGCTCGTGGCCAAAGTGGAAACAG  
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 25 CCGCAAGGAGAGCACTCAACCTCAAGAGAAAGAGAGATGATGATGTAACACTG  
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 >H\_1.0.0\_99143 Tp7c08.Xl Homo sapiens cDNA 3' end as: gi-11448929/// /clone=IMAGE:3644943  
 /clone\_end=3 /gb=BF436690 /gi-11448929 /ug=Hs.319750 /len=548.Weakly similar to DEHUC L-lactate  
 30 dehydrirogenase [gb:11.1.1.27] chain x - human [H. sapiens] [gml][UG][Hs#2910008] [SEQ ID No: 294]  
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 AGTGGGACTGCCCTGATCAGTGTGATGTCAGGCACTCTTCAACGCGTCAAGGTGGCGA  
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 55 >H\_1.0.0\_310 Homo sapiens cell-type T-cell immunoglobulin gamma chain, V region (IGHV) mRNA,  
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 65 >H\_1.0.0\_19016 Homo sapiens cysteine-rich, angiogenic inducer, 6L (CYR61), mRNA cr: gi-4504512///  
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TACTGGCATTCTGACACTATTTCCTCTTTTAATACACTTAACCTACGAGCCATTTTAAAG  
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5 >H\_1.0.0.41040 Homo sapiens cDNA FLJ40060 fis, clone TCOLM2000236, highly similar to P55-C-FOS  
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 65 CCGCTCTCGGAGAGCTCTTCTTGTAGAGAGTCTGAGGAGTCTGAGGAGTCTGAGGAGTCTT  
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70 GGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG  
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>gi|20270509|ref|NM|001158.1| Homo sapiens metallothionein 2 pseudogene 1 (processed) (MT2P1) on  
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>H\_1.0.0\_4048 Homo sapiens zuotin related factor 1 (ZRF1, mRNA cr: gi-22049761//  
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[Human jongleur 201102.252.C13]

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Figure 5

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[illegible]

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>M1.0.0.27805 Mus musculus similar to SI:PACKT90.L (novel protein) [Danio rerio] (LOC223845), mRNA  
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[illegible][illegible]

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AACACATAGCTTTTAAATTTGTGAAACAGACTTCTGCTCGTTACATTTTSCCTTTTA  
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 5 >gi|4505154|ref|NM|002402.1| Homo sapiens mesoderna specific transcript homolog (mouse) (MBST), mRNA  
 [SEQ ID NO: 89]  
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 >gi|16442925|gb|BB513945.2|BB513945 BB513945 RIKEN full-length enriched, 10 days lactation, adult  
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>|1892183|ref|NM|018685.1 Homo sapiens anillin, actin binding protein (scraps homolog,  
Drosophila) (ANLN) [582 ID No: 5]

GCTGGAAAGCCGAGAGAGACAGCTGTGTTGGAGATTCCTCCCGCTCAGACTCTCT

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W.1.9.11185 Mus musculus choline kinase (Chk), mRNA cr: gi-7304958//  
[mouse\_jorgleu, 201102, 6600, cl.] [880 ID NO: 99]

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&gt;H\_1.0.0\_15053 Homo sapiens hypothetical protein FLJ10815 (FLJ10815), mRNA cr: gi-89223921//

[Human\_jongleur\_201102.6327.C1] [SRQ ID NO: 103]

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&gt;gi|4483340|gb|AI550977.1|AI550977 vj19d05.y1 Barstead mouse irradiated colon MFLR87.Mus musculus

cDNA clone IMAGE:922185 5', mRNA sequence [SRQ ID NO: 104]

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CCCAATACAAATAAATGTAATAGTCAATA

&gt;H\_1.0.0\_37455 Homo sapiens mRNA for putative 40-6-3 protein si: gi-15216167///

[Human\_jongleur\_201102.cl.56.single] [SRQ ID NO: 105]

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>H\_1.0.0.2912 Homo sapiens interleukin 13 (IL13), mRNA cr: gi-4504644///

[Human\_g06142.c1: 2119..525, C1] [SBQ ID NO: 161]

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>H\_1.0.0.7164 Mus musculus killer cell lectin-like receptor subfamily A, member 21 (Klra21), mRNA

cr: gi-21361215/// [Mouse\_ongleur\_201102.3552.C9] [SBQ ID NO: 162]

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CAGCACTCATGTATGACACTTGGATCTCTGTCTCCCTCGGGTGTAAATGTGTGAGT  
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>H\_1.0.0.14332 Homo sapiens step II splicing factor SLU7 (SLU7), mRNA cr: gi-20127500///

[Human\_ongleur\_201102.5919.C1] [SBQ ID NO: 163]

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>H\_1.0.0.9637 Homo sapiens nuclear phosphoprotein similar to S. cerevisiae PWP1 (PWP1), mRNA cr: gi-  
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>M\_1.0.0.48190 BB032870 Mus musculus cDNA, 3' end as: gi-15403607// [clone=5830473M12 /clone\_end=3'  
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>NM\_1.0.0.6 62347 Moderately similar to P261\_MOUSE 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 1 (6PF-2/K/fru-2,6-P2ASE liver isozyme) [Includes: 6-phosphofructo-2-kinase; fructose-2,6-bisphosphatase] [M.musculus] acc:gi-15714162/// 603360763P1 Mus musculus cDNA, 5' end [clone=IMAGE:5368118 /clone\_end=5' /gib=BT737149 /gi=15714162 /ug=MM.132391 /len=896, /c1] [GI|MG|Mus2184367] [SEQ ID NO: 220]

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15 >H\_1.0.0.2410 Homo sapiens death-associated protein kinase 3 (DAPK3), mRNA cr: gi-4557510//  
[Human\_Jongleu.201102.336.C1] [SW ID NO: 228]  
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55 >H\_1.0.0.60877 Homo sapiens, KIAA0186 gene product, clone MGC:4333095, mRNA, complete  
cde 81; gb=15224811// [Human\_Jongleu.201102.612042.s1single] [SW ID NO: 229]  
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H\_1.0.0.11372 Moderately similar to H12207 hypothetical protein (B2 element) - mouse [M.musculus]  
as: gi-20165192/// UT-R-EJL-aka-c-14-0-UT.r1 Homo sapiens cDNA 5' end /clone=UI-E-EJL-aka-c-14-0-UT  
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232]

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TNRRRRRRRRRRRRRR  
>H\_1.0.0.5965 Homo sapiens serine (or cysteine) proteinase inhibitor, clade F (alpha-2 antipain, serpin,  
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[Human\_jongleur\_201102.1833.C1] [SQ ID NO: 233]

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TATCCCT

>H\_1.0.0.21590 Homo sapiens, similar to sphingosine kinase, clone MDC40267 IMAGE5213270, mRNA,  
complete cds cr: gi-22539642/// [Human\_jongleur\_201102.9905.C4] [SQ ID NO: 234]

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 +L\_1\_0\_1597 Homo sapiens (prosome, macrophage) inhibitor subunit 1 (P313) (PSM1), mRNA  
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>R\_1.0.0.4691 Homo sapiens, hypothetical protein similar to C37943, clone IMAGE:4827650, mRNA cr:  
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10 >M.1.0.0.19735 BB034567 Mus musculus cDNA, 3' end; cr: gi-15403646/// /clone=5830499F16 /clone\_end=1  
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>H.1.0.0.135942 Homo sapiens similar to data source:MGD, source key:MG1:102849,  
evidence:ISS-Kallickrein B, plasma 1-putative (LOC201859), mRNA as: gi-20472737//  
[gi|20472737|ref|XM\_114391.1|] [SEQ ID NO: 305]

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>gi|1988447|dbj|D49387.1|HUPB49FLB Human mRNA for NADP dependent leukotriene b4 12-  
5 GCMOxydehydrogenase, partial cds [SEQ ID NO: 306]

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>H.1.0.0.19867 Homo sapiens mitochondrial ribosomal protein S6 (MRP56), nuclear gene encoding  
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>H\_1.0.0.18527 Homo sapiens D-lactate dehydrogenase (LDHD), mRNA cr: gi-23821028//  
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>H\_1.0.0.10681 Homo sapiens methylene tetrahydrofolate dehydrogenase (MAD+ dependent),  
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 cr: gi-13699869// [Human\_jongleur\_201102.3990.C6] [SEQ ID NO: 310]  
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pR\_1.0.0.19410 Homo sapiens dipeptidase 1 (renal) (DPEP1), mRNA cr: gi-4758189//  
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 >H\_1.0.0.4048 Homo sapiens znuotin related factor 1 (ZRF1), mRNA cr: gi-22049761//  
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pH.1.0.0\_23435 Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 2  
15 (SLC22A2), mRNA; chr. 9: 45579561// (Human 5' UTR; 201102.11033.C1) [SEQ ID NO: 331]  
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>H\_1.0.0\_23435 Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 2 (SLC2A2), mRNA cr: gi-4557850/// [Human\_jongleur\_201102.11033.C1] [SBQ ID NO: 331]

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[Human joueur 201102.252.C13]

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